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OM nucleic - nucleic search, using sw model

Run on: March 21, 2005, 12:46:16 ; Search time 5666.07 seconds
(without alignments)
10732.529 Million cell updates/sec

Title: US-10-643-627-3

Perfect score: 1255
Sequence: 1 CGCTCCAGGCGCTGGTGTGACA.....TTAAGACCCCTATGAGT 1255

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb ba: *
2: gb htg: *
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7: gb ph: *
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9: gb pr: *
10: gb ro: *
11: gb sb: *
12: gb sy: *
13: gb un: *
14: gb vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1255	100.0	1255	6 AR012638	Sequence
2	1255	100.0	1255	6 AR171258	Sequence
3	1255	100.0	1255	6 AR171258	Sequence
4	1255	100.0	1255	6 AR171258	Sequence
5	1247	99.4	18351	9 AF400075	Homo sapi
6	1247	99.4	107278	9 AC114962	Homo sapi
7	1247	99.4	184536	2 AC068682	Homo sapi
8	1243.8	99.1	52358	9 AC010621	Homo sapi
9	1211	96.5	1289	9 HSPAR2B	H. sapiens p
10	1117	89.0	1451	6 CQ726252	Sequence
11	1117	89.0	2813	9 BC012453	Homo sapi
12	1115.4	88.9	2876	9 BC018130	Homo sapi
13	1114	88.8	1275	9 AY336105	Homo sapi
14	1113.8	88.7	1451	6 CQ870621	Sequence
15	1113.8	88.7	1451	6 CQ876753	Sequence
16	1113.8	88.7	1451	6 AX549014	Sequence
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19	1105.8	88.1	1414	6 AR012640	Sequence

20	1105.8	88.1	1414	6 AR171260	Sequence
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22	1105.4	88.1	1124	6 HSU3753	Human prote
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ALIGNMENTS

RESULT 1
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LOCUS AR012638
DEFINITION Sequence 3 from patent US 5763575.
ACCESSION AR012638
VERSION AR012638.1 GI:3970628
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1255)
AUTHORS Sundelin, J. and Scarborough, R.M.
TITLE Agonist and antagonist peptides of the C140 receptor
JOURNAL Patent: US 5763575-A 3 09-JUN-1998;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

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Best local similarity 100.0%; Pred. No. 0;
Matches 1255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	TGACTTTCATTTGAAACAACAGTGTACTGCTGAAACATTATTTCTGTAAGACCT 120	
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DB	121	TGCTCTCTCTCTCTCTGTAACGAACCAATGATCTCTTAAAGGAAGACCTTATGTTAA 180	
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DB	181	GGTTGATGACATCCAGCTGCACTGGAAGAGTTACAGTTGAACAGTCTTTCTGT 240	
QY	241	GGATGATTTTTCGACATCTGCTCACTGGAACCACTGCTCTCTTCCATTTGT 300	
DB	241	GGATGATTTTTCGACATCTGCTCACTGGAACCACTGCTCTCTTCCATTTGT 300	

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Db      421 CCTCTCTCTGTATCTGTGTTTCCCTTGAAGATTTGCTATCAATACATAGGCAACTG 480
QY      481 GATTATGAGGAGAGAGCTCTTTGTATGATGCTTATTTGGCTTTTCTATAGGCAACTG 540
Db      481 GATTATGAGGAGAGAGCTCTTTGTATGATGCTTATTTGGCTTTTCTATAGGCAACTG 540
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Db      541 TTCCATTTCTTTCATGACCTGCTCAGATGTCAGAGAGATTTGGGTATCGTGAACCCAT 600
QY      601 GGGGCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
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QY      901 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
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Db      1021 TGTCTATGAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
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Db      1141 CCGAAGATGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
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Db      1201 GAAATCAGAGCTTATCTTCAAGTTCAACCACTGTTAAGAGAGAGAGAGAGAGAG 1255

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RESULT 2
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LOCUS      ARI71258      1255 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6297026.
ACCESSION ARI71258
VERSION    ARI71258.1 GI:17910208

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KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1255)
AUTHORS     Sundelin, J. and Scarborough, R. M.
TITLE        Nucleic acids encoding the C140 receptor
JOURNAL      Patent: US 6297026-A 3 02-OCT-2001;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGCTCCAGGCTGGGTGACAGCGAGACCTGTCTCATTAATTAATAATGAATTAATGA 60
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Db      421 CCTCTCTCTGTATCTGTGTTTCCCTTGAAGATTTGCTATCAATACATAGGCAACTG 480
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Db      601 GGGGCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
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RESULT 3
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DEFINITION Sequence 3 from patent US 5629174.
ACCESSION 142455
VERSION 142455.1 GI:2467950
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1255)
AUTHORS Sundelin,J. and Scarborough,R.M.
TITLE Recombinant C140 receptor
JOURNAL Patent: US 5629174-A 3 13-MAY-1997;
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Source 1..1255
/organism="Unknown"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1141 CCGAAGTGTCCGCACTGTAAAGCATGATGCAAGTATCCCTCACTCAAGAAACATCCAG 1200
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DB 1201 GAAATCAGCTTTAATCTTCAAGTTCAACGCTTAAGACCTCCATTTGAGTT 1255

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DEFINITION Sequence 3 from patent US 5716789.
ACCESSION 187849
VERSION 187849.1 GI:3407789
KEYWORDS

SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 1255)
 TITLE Sundelin, J. and Scarborough, R.M.
 METHOD Method to determine ligands, agonist and antagonist of C140
 receptor.
 JOURNAL Patent: US 5716789-A 3 10-FEB-1998;
 FEATURES Location/Qualifiers
 source 1..1255
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ORIGIN

Query Match 100.0%; Score 1255; DB 6; Length 1255;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTCCAGGCTGGGTGACAGGAGACCTGTCTCATTAATTAATAATGAATGA 60
 DB 1 CGCTCCAGGCTGGGTGACAGGAGACCTGTCTCATTAATTAATAATGAATGA 60
 QY 61 TGTACTTTCAATTGAAACAACAGGTGTA CTGCTGAAAATTTATTTCTGTAAGACCT 120
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RESULT 5
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 LOCUS Homo sapiens coagulation factor II (thrombin) receptor-like 1
 DEFINITION (F2RL1) gene, complete cds.
 ACCESSION AF400075
 VERSION AF400075.1 GI:15021772
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 18351)
 AUTHORS Rieder, M.U., Carrington, D.P., Chung, M.-W., Lee, K.L., Poel, C.L.,
 Yi, Q. and Nickerson, D.A.
 TITLE Direct Submision
 JOURNAL Submitted (17-JUN-2001) Molecular Biotechnology, University of
 Washington, 1705 NE Pacific, Seattle, WA 98195, USA
 COMMENT To cite this work please use: SeattleSNPs, NHBI Program for
 Genomic Applications, UW-FHCRC, Seattle, WA (URL:
 http://pga.mbc.washington.edu)
 This sequence consists of 2 contigs. The gap between the contigs
 is represented as a run of N.
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 10775 10874: gap of unknown length
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[illegible]

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DEFINITION	Homo sapiens chromosome 5 clone RP11-206N2, complete sequence.			
ACCESSION	AC114962			
VERSION	AC114962.2 GI:24580362			
KEYWORDS	HTGS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission 1 (bases 1 to 107278)			
AUTHORS	Unpublished			
JOURNAL	2 (bases 1 to 107278)			
REFERENCE	DOE Joint Genome Institute.			
AUTHORS	Submitted (14-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
JOURNAL	3 (bases 1 to 107278) DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission Submitted (05-NOV-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Nov 5, 2002 this sequence version replaced gi:194224423. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov			
COMMENT	Finishing Completed at Stanford Human Genome Center www.sngc.stanford.edu Quality: Phrap Quality >=40 99.7% of Sequence; Estimated Total Number of Errors is 0.2. NOTE: This insert is not the entire sequence of the clone (entire sequence is 201.6kb). It is clipped at the overlaps with AC027342 and AC010621. The number of bases overlapped with AC027342 is 5439 and with AC010621 is 28528. Location/Qualifiers 1..107278 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="5" /clone="RP11-206N2"			
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source				

Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 167659 bases at least Q40
Consensus quality: 175736 bases at least Q30
Consensus quality: 178914 bases at least Q20
Insert size: 154000; agarose-fp
Insert size: 180936; sum-of-contigs
Quality coverage: 5.0 in Q20 bases; agarose-fp
Quality coverage: 4.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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source
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 ACCESSION Z49994
 VERSION Z49994.1 GI:1008086
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 AUTHORS Nystedt,S., Emlanson,K., Larsson,A.K., Strombeck,B. and Sundelin,J.
 TITLE Molecular cloning and functional expression of the gene encoding
 the human proteinase-activated receptor 2
 JOURNAL Eur. J. Biochem. 232 (1), 84-89 (1995)
 MEDLINE 96048032
 PUBMED 7556175
 REFERENCE 2 (bases 1 to 1289)
 AUTHORS Nystedt,S.
 TITLE Direct Submision
 JOURNAL Submitted (03-JUL-1995) Sverker Nystedt, Division of Neurobiology,
 The Wallenberg, Laboratory, Lund University, Soelvegatan 33A, Lund,
 S-223 62, Sweden
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RESULT 10
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DEFINITION Sequence 12186 from Patent WO02068579.
ACCESSION CQ726252
VERSION CQ726252.1 GI:42288766
KEYWORDS
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Mammalia; Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.
AUTHORS

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TITLE
Rlfe, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL
Patent: WO 02068579-A 12186 06-SEP-2002;
FEATUES
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DEFINITION      (CDNA clone MGC:9549 IMAGE:3857382), complete cds.
ACCESSION      BC012453
VERSION      BC012453.1
KEYWORDS      GI:15214649
SOURCE      MGC.
ORGANISM      Homo sapiens (human)

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REFERENCE
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2813)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altehus, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, U., Hsieh, F.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Ustun, T.B., Toshiyuki, S.,
Carinci, P., Prange, C., Raha, S.S., Loggiano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Ketterman, M., Madan, A., Rodriguez, S.,
Bouffard, G.G., Blakeley, R.W., Touchman, D.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schultz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,
Schurch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2813)
Strausberg, R.
Direct Submissions
Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu

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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louieged, R., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLI at: <http://image.lnli.gov>

Series: IRMA Place: 21 Row: D Column: 20

This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction. Similarity but not identity to protein.

FEATURES

source

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 Luo, W., Sedeblizade, F., Hanck, T. and Reiser, G.
 Human protease-activated receptor 2 (PAR-2)
 Unpublished
 2 (bases 1 to 1275)
 Luo, W., Sedeblizade, F., Hanck, T. and Reiser, G.
 Direct Submision
 Submitted (04-JUL-2003) Medical Faculty, Institute of
 Neurobiochemistry, Leipziger Str. 44, Magdeburg, Saxony-Anhalt
 39120, Germany

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 AUTHORS
 RTTLR
 JOURNAL
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RESULT 15
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LOCUS CQ876755
DEFINITION Sequence 1 from Patent WO2004080373.
ACCESSION CQ876755
VERSION CQ876755.1 GI:53790207
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Golz,S., Brueggemeier,U. and Summer,H.
TITLES Diagnostics and therapeutics for diseases associated with g-protein
coupled proteinase activated receptor 2 (par2)
JOURNAL Patent: WO 2004080373-A 1 23-SEP-2004;
Bayer Healthcare AG (DE)
FEATURES
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1..1451
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 88.7%; Score 1113.8; DB 6; Length 1451;
Best Local Similarity 99.8%; Pred. No. 6e-305; Indels 0; Gaps 0;
Matches 1115; Conservative 0; Mismatches 2;

QY 139 AGGACCAATAGATCTCTTAAGAAAGAGCCCTTATTTGTAAGTGGATGGACATCCCA 198
Db 228 AGGACCAATAGATCTCTTAAGAAAGAGCCCTTATTTGTAAGTGGATGGACATCCCA 287
QY 199 CGTCACTGAAAAAGATTACAGTTGAACAGCTTTTCTGTGATGAGTTTCTGCATC 258
Db 288 CGTCACTGAAAAAGATTACAGTTGAACAGCTTTTCTGTGATGAGTTTCTGCATC 347
QY 259 TGTCTCACTGAAAACTGACCACTGTCTTCTTCAATTGTCTACCAATTGTGTGT 318
Db 348 TGTCTCACTGAAAACTGACCACTGTCTTCTTCAATTGTCTACCAATTGTGTGT 407
QY 319 GGTGGGTTTGGCAAGTAAGGCAATGGCCGTGGGTCTTCTTTCCGAATGAAGAA 378
Db 408 GGTGGGTTTGGCAAGTAAGGCAATGGCCGTGGGTCTTCTTTCCGAATGAAGAA 467
QY 379 GCACCTGTGTGATTTACATGGCCAATCTGGCTTGGCTGACCTCTCTGTCACTG 438
Db 468 GCACCTGTGTGATTTACATGGCCAATCTGGCTTGGCTGACCTCTCTGTCACTG 527
QY 439 GTTCCCTTGAAGATTGCTTATCATCATATGAGCAACACTGATTTATGGGAAGCTCT 498

Db 528 GTTCCCTTGAAGATTGCTTATCATCATATGAGCAACACTGATTTATGGGAAGCTCT 587
QY 499 TGTAAATGCTTAATTTGCTTTTCTATGGAACAATGATCTGTCCATCTCTTCAATGAC 558
Db 588 TGTAAATGCTTAATTTGCTTTTCTATGGAACAATGATCTGTCCATCTCTTCAATGAC 647
QY 559 CTGCTCACTGTGACAGAGTATTTGGTCAATCGTGAACCCCATGGGCACTCCAGAGAA 618
Db 648 CTGCTCACTGTGACAGAGTATTTGGTCAATCGTGAACCCCATGGGCACTCCAGAGAA 707
QY 619 GGCAAACTTGGCATTTGGATCTCCCTGGCAATATGGGCTGATTTCTGTGGTACCAT 678
Db 708 GGCAAACTTGGCATTTGGATCTCCCTGGCAATATGGGCTGATTTCTGTGGTACCAT 767
QY 679 CCTTTGATGTGCTGAACAGACCATCTTCAATTCCTGCTGGAACATCAGACCTGTCA 738
Db 768 CCTTTGATGTGCTGAACAGACCATCTTCAATTCCTGCTGGAACATCAGACCTGTCA 827
QY 739 TGAATTTTGCCTGACAGACTTTGGTGGAGACATGTCAATTACTTCTCTCTGGC 798
Db 828 TGAATTTTGCCTGACAGACTTTGGTGGAGACATGTCAATTACTTCTCTCTGGC 887
QY 799 CATGGGGTCTTCTGTTCCAGGCTTCTCAAGCTGTGCTATGTGCTGATGATCAG 858
Db 888 CATGGGGTCTTCTGTTCCAGGCTTCTCAAGCTGTGCTATGTGCTGATGATCAG 947
QY 859 AATGCTGCATCTTCTGCATGATGAATACTCAGAGAAAGAAAGAGAGGCCATCA 918
Db 948 AATGCTGCATCTTCTGCATGATGAATACTCAGAGAAAGAAAGAGAGGCCATCA 1007
QY 919 ACTGATTTGACTGTCTGCGCATGTACTGATCTGCTTCACTCTTATTAACCTTGTGCT 978
Db 1008 ACTGATTTGACTGTCTGCGCATGTACTGATCTGCTTCACTCTTATTAACCTTGTGCT 1067
QY 979 TGTGTCATTAATTTCTGATTAAGACGAGGCGACAGGACATGTCTATGCCCTGATAC 1038
Db 1068 TGTGTCATTAATTTCTGATTAAGACGAGGCGACAGGACATGTCTATGCCCTGATAC 1127
QY 1039 TGTAGCCCTCTGCTCTCTCAACCTTAAACAGCTGCATCGACCCCTTGTCTATTACTTTGT 1098
Db 1128 TGTAGCCCTCTGCTCTCTCAACCTTAAACAGCTGCATCGACCCCTTGTCTATTACTTTGT 1187
QY 1099 TTCACATGATTTACAGGATCAGCAAGAAAGCTCTCTTGGCGAAGTCCGCACTGT 1158
Db 1188 TTCACATGATTTACAGGATCAGCAAGAAAGCTCTCTTGGCGAAGTCCGCACTGT 1247
QY 1159 AAAGCAGATGCAAGTATCCCTCACTCAAGAAACACTCCAGGAATCCAGCTCTTACTC 1218
Db 1248 AAAGCAGATGCAAGTATCCCTCACTCAAGAAACACTCCAGGAATCCAGCTCTTACTC 1307
QY 1219 TTCAGTTCAACCACTGTTAAAGACTCTTATTTGAGTT 1255
Db 1308 TTCAGTTCAACCACTGTTAAAGACTCTTATTTGAGTT 1344

Search completed: March 21, 2005, 21:39:45
Job time : 5676.07 secs

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OM protein - protein search, using sw model

Run on: March 18, 2005, 20:59:39 ; Search time 69.0868 Seconds
(without alignments)
2228.076 Million cell updates/sec

Title: US-10-643-627-4

Perfect score: 2030
Sequence: 1 MNTLSPFGQTSVTAETFTISW.....KHSRKSSVSSTSTVTKTSY 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	2030	100.0	398	2	AAR66921	Aar66921 Human C14
2	2030	100.0	398	2	AAW01953	Aaw01953 Human C14
3	1903	93.7	397	3	AAH35641	Aah35641 Human PAR
4	1903	93.7	397	5	AAE26678	Aae26678 Human coa
5	1903	93.7	397	6	ABG73508	Abg73508 Human par
6	1903	93.7	397	7	ABE62812	Abg62812 Human par
7	1903	93.7	397	8	ADO29311	Ado29311 Human GPC
8	1903	93.7	397	8	ADG574020	Adg574020 Human G-P
9	1898	93.5	397	8	ADL61221	Adl61221 Human coa
10	1897	93.4	397	6	ABP81907	Abp81907 Human pro
11	1897	93.4	397	7	ADK52594	Adk52594 Hematolog
12	1897	93.4	397	7	ADN39997	Adn39997 Cancer/an
13	1897	93.4	397	8	ADR46675	Adr46675 Cancer-as
14	1872	92.2	397	2	AAR66923	Aar66923 Human C14
15	1872	92.2	397	2	AAW01955	Aaw01955 Human C14
16	1865.5	91.9	394	2	AAW51408	Aaw51408 Human pro
17	1816	89.5	355	8	AD128653	Ad128653 Human mod
18	1789.5	88.2	389	8	ADO28601	Ado28601 Human PAR
19	1743	85.9	341	8	AD128654	Ad128654 Human mod
20	1706.5	84.1	395	2	AAR66920	Aar66920 Murine C1
21	1701.5	83.8	395	2	AAW01952	Aaw01952 Murine C1
22	1672	82.4	399	2	AAR66922	Aar66922 Murine C1
23	1672	82.4	399	2	AAW01954	Aaw01954 Murine C1
24	1672	82.4	399	7	ABR63562	Abg63562 Delayed h
25	1672	82.4	399	8	ADO29312	Ado29312 Mouse GPC

26	1652	81.4	397	7	ADG62810	Adg62810 Rat Prote
27	1643	80.9	330	8	AD128655	Ad128655 Human mod
28	1620	30.5	430	8	ADO29310	Ado29310 Mouse GPC
29	619	30.5	425	2	AAR27240	Aar27240 Human thr
30	619	30.5	425	2	AAR60698	Aar60698 Fragment
31	619	30.5	425	2	AAW51407	Aaw51407 Human pro
32	619	30.5	425	2	AAV49570	Aay49570 Human thr
33	619	30.5	425	5	AAH17032	Aah17032 Human thr
34	619	30.5	425	5	AAH60697	Aag60697 Human thr
35	619	30.5	425	6	ABG73511	Abg73511 Human thr
36	619	30.5	425	6	ABR47449	Abt47449 Breast ca
37	619	30.5	425	6	ABP81919	Abp81919 Human thr
38	619	30.5	425	7	ADG89876	Adg89876 Human coa
39	619	30.5	425	8	ADL14208	Adl14208 Novel hum
40	619	30.5	425	8	ADN04016	Adn04016 Antipori
41	619	30.5	425	8	ADO29309	Ado29309 Human GPC
42	619	30.5	425	8	ADQ18985	Adq18985 Human bot
43	619	30.5	425	8	ADR45608	Adr45608 Human G P
44	619	30.5	425	8	ADG84489	Adg84489 Human pro
45	619	30.5	426	3	AAV45035	Aay45035 Human thr

ALIGNMENTS

RESULT 1	
AAAR66921	AAAR66921 standard; protein; 398 AA.
XX	XX
AC	AAAR66921;
XX	XX
DT	25-MAR-2003 (revised)
DT	22-AUG-1995 (first entry)
XX	XX
DE	Human C140 receptor.
XX	XX
KM	G-protein-coupled receptor; G-protein; C140 receptor.
XX	XX
OS	Homo sapiens.
XX	XX
PH	Key
FT	Protein
FT	Location/Qualifiers
FT	/label= signal peptide
FT	11..132
FT	/label= transmembrane II
FT	31
FT	/label= Asn linked glycosylation site
FT	37..38
FT	/label= protease receptor cleavage site
FT	81..103
FT	/label= transmembrane I
FT	150..174
FT	/label= transmembrane III
FT	191..212
FT	/label= transmembrane IV
FT	223
FT	/label= Asn linked glycosylation site
FT	245..267
FT	/label= transmembrane V
FT	289..309
FT	/label= transmembrane VI
FT	327..348
FT	/label= transmembrane VII
XX	XX
PN	WO9503318-A1.
XX	XX
PD	02-FEB-1995.
XX	XX
PR	26-JUL-1994; 94MO-US008536.
XX	XX
PR	26-JUL-1993; 93US-00097938.
XX	XX
PA	(CORT-) COR THERAPEUTICS.

XX Scarborough RM, Sundelin J;
 PI WPI: 1995-075182/10.
 DR N-PSDB; AA084558.
 XX
 PT New DNA encoding recombinant C140 receptor - and novel agonists and
 PT antagonists and specific antibodies with therapeutic and diagnostic
 PT applications.
 XX
 PS Disclosure; Fig 2; 57pp; English.
 CC The availability of genomic DNA encoding the mouse protease C140 receptor
 CC (see Q84557) permitted the retrieval of the corresp. human gene. A human
 CC genomic library cloned in the vector EMBL3 was screened using the entire
 CC coding region of the murine clone as a probe. The recovered human gene
 CC including the DNA sequence and the deduced AA sequence are shown in
 CC Q84558 & R68921. Subsequent experiments indicated that the human C140
 CC gene is located in the same region of the long arm of chromosome number 5
 CC (5q12-5q13) as has been reported for the human thrombin receptor gene.
 CC (Updated on 25-MAR-2003 to correct PM field.)
 CC
 XX
 SQ Sequence 398 AA;
 Query Match 100.0%; Score 2030; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 5.6e-210;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNVLSEQGSVTAETATISVWTLVPLSCGTGNNSSKGRSLGKVDGSHVTKGVETVP 60
 DB 1 MNVLSEQGSVTAETATISVWTLVPLSCGTGNNSSKGRSLGKVDGSHVTKGVETVP 60
 QY 61 SVDEFSASVLTGKLTVPFPIVTVIVVVGLPENGMALWFLFRTKKKHPAVIYMANIAL 120
 DB 61 SVDEFSASVLTGKLTVPFPIVTVIVVVGLPENGMALWFLFRTKKKHPAVIYMANIAL 120
 QY 121 ADLSVIMPEPLKTAHYHGNMWTYGERALCNVLIGFFYGNMYSILFMTCLSVORVYIVN 180
 DB 121 ADLSVIMPEPLKTAHYHGNMWTYGERALCNVLIGFFYGNMYSILFMTCLSVORVYIVN 180
 QY 181 PMGSKRKKNIAIGISLAWLILVLTIPLYVVKOTIFPALMTTCCHDVLPEQLLVGDM 240
 DB 181 PMGSKRKKNIAIGISLAWLILVLTIPLYVVKOTIFPALMTTCCHDVLPEQLLVGDM 240
 QY 241 FNFYFLSLATGVPFLPAPFLTASAVYLMIRMLRSSAMDESSKKKKRAIKLIVTLAMYLIC 300
 DB 241 FNFYFLSLATGVPFLPAPFLTASAVYLMIRMLRSSAMDESSKKKKRAIKLIVTLAMYLIC 300
 QY 301 FTFSNLLLVVHYFLIKSGQSHVYALYVALCLSTNSCIDPVTYVFSHDPDHAKNAL 360
 DB 301 FTFSNLLLVVHYFLIKSGQSHVYALYVALCLSTNSCIDPVTYVFSHDPDHAKNAL 360
 QY 361 LCRSVRTVKOMQVSLTSSKGRSSSYSSSTTVKTSY 398
 DB 361 LCRSVRTVKOMQVSLTSSKGRSSSYSSSTTVKTSY 398
 RESULT 2
 AA01953
 ID AA01953 standard; protein; 398 AA.
 XX
 AC AA01953;
 XX
 DT 01-APR-1997 (first entry)
 XX
 DE Human C140 receptor, with putative signal sequence.
 XX
 KM C140 receptor; G-protein linked; coupled; seven pass; agonist;
 KM antagonist; hypertension; hypotension; blood pressure.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT Peptide 1..27
 FT /note= "putative signal peptide, differs from signal
 FT peptide encoded by a cDNA clone of this receptor (see
 FT AA01955), the signal sequence given for the cDNA clone
 FT is believed to be the correct sequence"
 FT 28..398
 FT Protein
 FT /note= "mature protein"
 FT 31
 FT Modified-site
 FT /note= "potential Asn-linked glycosylation site"
 FT 37..38
 FT Cleavage-site
 FT /note= "putative protease receptor cleavage site"
 FT 81..103
 FT Region
 FT /note= "transmembrane region I"
 FT 111..132
 FT Region
 FT /note= "transmembrane region II"
 FT 151..174
 FT Region
 FT /note= "transmembrane region III"
 FT 191..212
 FT Region
 FT /note= "transmembrane region IV"
 FT 223
 FT Modified-site
 FT /note= "potential Asn-linked glycosylation site"
 FT 245..267
 FT Region
 FT /note= "transmembrane region V"
 FT 289..309
 FT Region
 FT /note= "transmembrane region VI"
 FT 327..348
 FT Region
 FT /note= "transmembrane region VII"
 XX
 PN W09623225-A1.
 XX
 XX 01-AUG-1996.
 PD
 XX
 XX 25-JAN-1996; 96WO-US001179.
 PF
 XX
 XX 25-JUN-1995; 95US-00390301.
 PR
 XX
 PA (COR-) COR THERAPEUTICS INC.
 XX
 PI Sundelin J, Scarborough RM;
 XX
 DR WPI: 1996-362813/36.
 DR N-PSDB; AAT32037.
 XX
 PT Vector for expression C140 cell surface receptor in host cell - useful to
 PT identify C140 agonist and antagonists, which are antihypertensives and
 PT elevators of blood pressure, respectively.
 XX
 PS Example 2; Fig 2A-B; 60pp; English.
 XX
 CC AA01953 represents the human C140 receptor (C140R), including a putative
 CC signal peptide (see features table). DNA encoding C140R may be engineered
 CC so as to allow the recombinant expression of C140R in a suitable host
 CC cell, i.e. by removing the native expression-control sequences and
 CC replacing them with control sequences operable in the host. Such a
 CC recombinant receptor can be expressed on the surface of oocytes, this
 CC provides a good assay system for identifying agonists/antagonists of
 CC C140R. The C140 receptor is a G-protein linked receptor and a member of
 CC the "seven-pass" transmembrane receptor superfamily (peptide chain of the
 CC transmembrane regions within the cell membrane seven times, producing seven
 CC transmembrane regions within the receptor molecule). The C140 receptor is
 CC involved in controlling blood pressure. C140 antagonists (see AA01942-
 CC W01951) are useful to inhibit signalling from this receptor, resulting in
 CC an increase in blood pressure and are therefore useful in pharmaceuticals
 CC for the treatment of hypotension (low blood pressure). Conversely
 CC agonists (see AA01941-W01941) of C140 are useful in pharmaceuticals for
 CC the treatment of hypertension (high blood pressure)
 XX
 SQ Sequence 398 AA;
 Query Match 100.0%; Score 2030; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 5.6e-210;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PT of F2RL1 and treating disorders associated with abnormal expression or
PT function of F2RL1.
XX Claim 27; Fig 3; 65pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising genes and
CC haplotypes of the coagulation factor II (thrombin) receptor like 1
CC (F2RL1) gene. Polymorphic variants of the F2RL1 gene are useful in
CC studying the expression and biological function of F2RL1, and in
CC identifying drugs targeting F2RL1 protein for treating disorders
CC associated with abnormal expression or function of F2RL1, e.g. asthma,
CC chronic pulmonary disease, and inflammatory disorders. Polynucleotides
CC comprising a polymorphic gene variant or fragment may be used for
CC therapeutic purposes, where a patient could benefit from expression or
CC increased expression of a particular F2RL1 protein isoform, or an
CC expression vector encoding the isoform may be administered to the
CC patient. Haplotype information is useful in improving the efficiency and
CC output of several steps in drug discovery and development process,
CC including target validation, identifying lead compounds, and early phase
CC clinical trials. Information on polymorphisms may be applied in studying
CC biological functions of F2RL1 as well as in identifying drugs targeting
CC this protein for the treatment of disorders related to its abnormal
CC expression or function. The invention is useful in gene therapy. The
CC present sequence is human F2RL1 protein
XX
XX Sequence 397 AA;
SQ
Query Match 93.7%; Score 1903; DB 5; Length 397;
Best Local Similarity 96.9%; Pred. No. 2.9e-196;
Matches 373; Conservative 4; Mismatches 4; Indels 4; Gaps 1;
QY 18 SVNTLVFVLSCT---GTNSSKGRSLIGKVDGTSHTGKGVTVTVFSVDEFSASVLTGK 73
DB 13 AILAAASLSCSGTIOGTNSSSKGRSLIGKVDGTSHTGKGVTVTVFSVDEFSASVLTGK 72
QY 74 LTTVFLPIYTTIVFVVGLPNSGMAWVFLFRTKKHPAVIYMANLADLSTIWPPLKI 133
DB 73 LTTVFLPIYTTIVFVVGLPNSGMAWVFLFRTKKHPAVIYMANLADLSTIWPPLKI 132
QY 134 AYHIHGNMNIYGBALCNVLIGFFYGNMYSILFMTCLSVQRVWVYVNPMSHKKANIAI 193
DB 133 AYHIHGNMNIYGBALCNVLIGFFYGNMYSILFMTCLSVQRVWVYVNPMSHKKANIAI 192
QY 194 GISLAIWLLILVTLPIYVVKQTFIPALNITTCDDVLEQOLLVGMFVPSLAIQVFL 253
DB 193 GISLAIWLLILVTLPIYVVKQTFIPALNITTCDDVLEQOLLVGMFVPSLAIQVFL 252
QY 254 PPAFLTASAYVLMIRLRSSADENSEKKRKAIKLIVTLAMYLICFPNSNLLVVHYF 313
DB 253 PPAFLTASAYVLMIRLRSSADENSEKKRKAIKLIVTLAMYLICFPNSNLLVVHYF 312
QY 314 LKISQOSHYVALYIYALCLSTLNSCIDPFVYFVSHDFRDAKNAALLCRSVTVKQMOV 373
DB 313 LKISQOSHYVALYIYALCLSTLNSCIDPFVYFVSHDFRDAKNAALLCRSVTVKQMOV 372
QY 374 SLTSKGRSRKSSSYSSSTTVTKTSY 398
DB 373 SLTSKGRSRKSSSYSSSTTVTKTSY 397
RESULT 5
ABG73508 standard; protein; 397 AA.
XX
XX ABG73508;
XX
XX 14-FEB-2003 (first entry)
XX
XX Human par2 protein SEQ ID 39.
XX
XX G-protein coupled receptor; HGPBRMY1; HGPBRMY2; immunosuppressive;
XX Cardiac; neuroprotective; antiinflammatory; cycostatic; vulnerrary;
XX vaccine; gene therapy; autoimmune; cardiovascular; neural; reproductive;

KW haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
KW birth defect; aberrant phosphorylation; acute phase response; receptor;
KW signal transduction; hyperimmune activity; inflammatory; hypercongenital;
KW necrotic lesion; wound; organ transplant rejection.
XX
OS Homo sapiens.
XX
PN WO200268591-A2.
XX
PD 06-SEP-2002.
XX
XX 22-FEB-2002; 2002WO-US005281.
XX
XX 23-FEB-2001; 2001US-0270792P.
XX 23-FEB-2001; 2001US-0270793P.
XX 06-JUN-2001; 2001US-0296427P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Feder J, Ramanathan C, Nelson T, Mintier G, Cacace A, Barber L;
PI Kornacker M, Bol D;
XX
XX WPI; 2003-058304/05.
XX
XX New human HGPBRMY1 or HGPBRMY2 polynucleotide and polypeptide, useful
PT preventing, treating or ameliorating a disorder e.g., wound,
PT cardiovascular disorder or transplant rejection.
XX
XX Disclosure; Fig 4; 316pp; English.
XX
CC This invention describes the novel human G-protein coupled receptors
CC (GPCR's), HGPBRMY1 or HGPBRMY2 which have immunosuppressive, cardiac,
CC neuroprotective, antiinflammatory, cycostatic and vulnerary activity and
CC can be used in vaccines or for gene therapy. Pharmaceutical compositions
CC comprising HGPBRMY1 or HGPBRMY2 polypeptides or their agonists or
CC antagonists or modulators, or a HGPBRMY1- or HGPBRMY2-specific antibody
CC are useful for preventing, treating or ameliorating a medical condition
CC comprising autoimmune, cardiovascular, neural, reproductive,
CC haematopoietic, pulmonary, gastrointestinal or proliferating disorder, a
CC cell cycle or birth defect, a disorder related to aberrant
CC phosphorylation, acute phase responses or signal transduction or to
CC hyperimmune activity, an inflammatory or hypercongenital condition, a
CC necrotic lesion, a wound, organ transplant rejection or a condition
CC related to organ transplant rejection. This sequence represents a G-
CC protein coupled receptor associated with the human HGPBRMY proteins
CC described in the disclosure of the invention
XX
SQ Sequence 397 AA;
Query Match 93.7%; Score 1903; DB 6; Length 397;
Best Local Similarity 96.9%; Pred. No. 2.9e-196;
Matches 373; Conservative 4; Mismatches 4; Indels 4; Gaps 1;
QY 18 SVNTLVFVLSCT---GTNSSKGRSLIGKVDGTSHTGKGVTVTVFSVDEFSASVLTGK 73
DB 13 AILAAASLSCSGTIOGTNSSSKGRSLIGKVDGTSHTGKGVTVTVFSVDEFSASVLTGK 72
QY 74 LTTVFLPIYTTIVFVVGLPNSGMAWVFLFRTKKHPAVIYMANLADLSTIWPPLKI 133
DB 73 LTTVFLPIYTTIVFVVGLPNSGMAWVFLFRTKKHPAVIYMANLADLSTIWPPLKI 132
QY 134 AYHIHGNMNIYGBALCNVLIGFFYGNMYSILFMTCLSVQRVWVYVNPMSHKKANIAI 193
DB 133 AYHIHGNMNIYGBALCNVLIGFFYGNMYSILFMTCLSVQRVWVYVNPMSHKKANIAI 192
QY 194 GISLAIWLLILVTLPIYVVKQTFIPALNITTCDDVLEQOLLVGMFVPSLAIQVFL 253
DB 193 GISLAIWLLILVTLPIYVVKQTFIPALNITTCDDVLEQOLLVGMFVPSLAIQVFL 252
QY 254 PPAFLTASAYVLMIRLRSSADENSEKKRKAIKLIVTLAMYLICFPNSNLLVVHYF 313
DB 253 PPAFLTASAYVLMIRLRSSADENSEKKRKAIKLIVTLAMYLICFPNSNLLVVHYF 312

QY 314 LINKOGSHVYALYVALCSTLNSCIDPFVYVYFVSHDFRDHAKNALCGRSVRTVKOMOV 373
 DB 313 LINKOGSHVYALYVALCSTLNSCIDPFVYVYFVSHDFRDHAKNALCGRSVRTVKOMOV 372
 QY 374 SLTSKSHSRKSSSYSSSSTTVKTSY 398
 DB 373 SLTSKSHSRKSSSYSSSSTTVKTSY 397

RESULT 6
 ADB62812
 ID ADB62812 standard; protein; 397 AA.
 XX
 AC ADB62812;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P55085, SEQ ID NO 8745.
 XX
 KM Human pain; neuronal tissue; gene therapy;
 KM spinal segmental nerve injury; chronic constriction injury; CCI;
 KM spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002MO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-033347P.
 XX
 PA (GEMO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'Urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; P55085.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017P; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SO Sequence 397 AA;
 QY Query Match 93.7%; Score 1903; DB 7; Length 397;
 DB Best Local Similarity 96.9%; Pred. No. 2.9e-196;
 Matches 373; Conservative 4; Mismatches 4; Indels 4; Gaps 1;
 QY 18 SVMTLVFLSCT----GMRSSKGRSLIGKVDGSHVGTGKVTYVTSVNDFFASVYTGK 73
 DB 13 AILAAASLSCSGTIGTNRSSKGRSLIGKVDGSHVGTGKVTYVTSVNDFFASVYTGK 72
 QY 74 LTVVFLPIVYTVIVFVGLPSNGMALWVFLPRTKKGGPAVITYMANIALADLLSVIPLKI 133
 DB 73 LTVVFLPIVYTVIVFVGLPSNGMALWVFLPRTKKGGPAVITYMANIALADLLSVIPLKI 132.
 QY 134 AYHIGNMWIYGBALCNVLIGFYGNNYCSILFWTCLSVORVYVIVNPMGHSRKKANIAI 193
 DB 133 AYHIGNMWIYGBALCNVLIGFYGNNYCSILFWTCLSVORVYVIVNPMGHSRKKANIAI 192
 QY 194 GISLAIWLLILVTIPYVVKQTFIPALNITTCDDVLPQOLLVGMFRTPLSAIGVPL 253
 DB 193 GISLAIWLLILVTIPYVVKQTFIPALNITTCDDVLPQOLLVGMFRTPLSAIGVPL 252
 QY 254 PPAFLTASAVYVLMIRMLRSSAMDESEKRRKRAIKLIVTLAMVYLIGFTPSNLLVYHYF 313
 DB 253 PPAFLTASAVYVLMIRMLRSSAMDESEKRRKRAIKLIVTLAMVYLIGFTPSNLLVYHYF 312
 QY 314 LINKOGSHVYALYVALCSTLNSCIDPFVYVYFVSHDFRDHAKNALCGRSVRTVKOMOV 373
 DB 313 LINKOGSHVYALYVALCSTLNSCIDPFVYVYFVSHDFRDHAKNALCGRSVRTVKOMOV 372
 QY 374 SLTSKSHSRKSSSYSSSSTTVKTSY 398
 DB 373 SLTSKSHSRKSSSYSSSSTTVKTSY 397

RESULT 7
 ADO29311
 ID ADO29311 standard; protein; 397 AA.
 XX
 AC ADO29311;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human GPCR F2RL1, SEQ ID NO:412.
 XX
 KM G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KM transgenic mouse; neurological disorder; adrenal gland disorder;
 KM colon disorder; intestinal disorder; cardiovascular disorder;
 KM muscular disorder; blood disorder; immune disorder; bone disorder;
 KM joint disorder; metabolic disorder; nutritive disorder; cancer;
 KM kidney disorder; liver disorder; lung disorder; breast disorder;
 KM ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KM skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KM thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;
 KM cytoskeletal; antiinflammatory; vasoprotic; antianginal; antiarrhythmic;
 KM CNS; central nervous system; respiratory; antidiabetic; antidiabetic;
 KM virucide; hepatotropic; antibacterial; antineoplastic; antiseborrhoeic;
 KM dermatological; antidiabetic; antihypertensive; anorectic;
 KM immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;
 KM receptor.
 XX
 XX Homo sapiens.
 OS
 PN WO2004040000-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 09-SEP-2003; 2003MO-US028226.
 XX
 PR 09-SEP-2002; 2002US-0409303P.

PR	09-APR-2003; 2003US-0461329P.
XX	(PRIM-) PRIMAL INC.
XX	Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li P,
P1	Madsen L, McLwain XL, Pavlova MN, Vassiliadis D, Zeng H;
XX	WPI; 2004-390329/36.
DR	N-PSDB; ADO29874.
PT	Novel mammalian G protein coupled receptors, useful for identifying
PT	compounds that modulates diagnosing and treating disease condition
PT	associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT	pectoris, Parkinson's disease.
XX	Claim 151; SEQ ID NO 412; 542bp; English.
PS	The invention relates to human and mouse G protein-coupled receptors
CC	(GPCRs) and nucleic acids encoding them. The invention also relates to
CC	sequences at least 90% identical to the GPCR proteins and nucleic acids
CC	of the invention; methods of treating, preventing or diagnosing diseases
CC	associated with GPCRs of the invention; methods of screening for
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC	from the transgenic mice; kits comprising several mice, each of which has
CC	a mutation in a different GPCR gene of the invention; and kits comprising
CC	probes which hybridize to GPCR polynucleotides of the invention. The
CC	invention further discloses variants of the GPCR polypeptides and vectors
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC	be used in the diagnosis, treatment or prevention of a wide variety of
CC	diseases including neurological disorders (e.g., Alzheimer's disease,
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC	disorders of the adrenal gland; disorders of the colon or intestine
CC	(e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC	syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC	myocardial infarction); muscular disorders; blood disorders (e.g.,
CC	anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC	AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC	arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC	obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC	diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC	uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC	thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC	invention. Note: The full sequence data for this patent did not form part
CC	of the printed specification; those sequences not shown were obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 397 AA;
Query Match	93.7%; Score 1903; DB 8; Length 397;
Best Local Similarity	96.9%; Pred. No. 2.9e-196;
Matches 373; Conservative	4; Mismatches 4; Indels 4; Gaps 1
18 SWMTLVFLSCT-----GTNRSSKGRSLIGKVDTSHVTKGVTVETVFSYDERFSASVLTKG	73
:::::	
13 AIIAASISCSGTIGTNRSSKGRSLIGKVDTSHVTKGVTVETVFSYDERFSASVLTKG	72
74 LTTVEPLPVYTIVFVVGGLPSNGMALMVFIFRYKKGPATVYMANALADLSVIWFELKI	133
Db 73 LTTVELPIVTITVFVVGGLPSNGMALMVFIFRYKKGPATVYMANALADLSVIWFELKI	132
QY AVHIGNNMVIGEALCNVLIGFFYGNYMSILFMTCLSVRQVWVINVPMGHRRKANAI	193
Db 133 AHVHGNMMVIGEALCNVLIGFFYGNYMSILFMTCLSVRQVWVINVPMGHRRKANAI	192
QY GISLAIWLILLYTIVPLVYVKOTIFIPALNITTCHDVLPBEOLLVGDMEFYFSLAIGVEL	253
Db 193 GISLAIWILLILLYTIVPLVYVKOTIFIPALNITTCHDVLPBEOLLVGDMEFYFSLAIGVEL	252
QY PPAPLTAAAYVMIMRLRSSANDENSEKKRKAKIIVTLVLMYYLICFTPSNILLVHYAF	313

Db	253	PFAPIFLTSAYVLMIRMLRSSAMDENSEKKRRKALKIVTLAMTILICTPBNLLVVHYF	312
Oy	314	LIKSGQSHVVALYIVALCTSTLNSCIDPFYYTVFSHDPRDHAKNALLCRSVRTVKOMOV	373
Db	313	LIKSGQSHVVALYIVALCTSTLNSCIDPFYYTFVSHDFRDHAKNALLCRSVRTVKOMOV	372
Oy	374	SLTSKHSKRKSSSYSSSSTTYKTISY	398
Db	373	SLTSKHSKRKSSSYSSSSETTYKTISY	397
 RESULT 8 ADST74020 ID ADST74020 standard; protein; 397 AA. XX AC ADST74020; XX DT 16-DEC-2004 (first entry) XX DE Human G-protein coupled proteinase activated receptor 2 (PAR2). XX KW Human; proteinase activated receptor 2; PAR2; G-protein coupled receptor; KM receptor; cardiac; neuroprotective; nephrotropic; respiratory-gen.; XX gastrointestinal-gen.; gene therapy. OS Homo sapiens. XX PN WO2004080373-A2. XX PD 23-SEP-2004. XX PF 26-FEB-2004; 2004WO-EP001896. XX PR 11-MAR-2003; 2003EP-00004980. PA (FARB) BAYER HEALTHCARE AG. XX PI Golz S, Brueggemeier U, Summer H; XX DR WPI; 2004-677358/66. XX DR N-PSTDB; ADST74019. XX PT Screening for therapeutic agents for treating e.g., cardiovascular PT diseases by contacting a test compound with a proteinase activated PT receptor 2 (PAR2) polypeptide or polynucleotide and detecting binding of PT the test compound. XX PS Disclosure; SEQ ID NO 2; 121bp; English. XX PS The present sequence is that of human G-protein coupled proteinase CC activated receptor 2 (PAR2). PAR2 is an antiinflammatory receptor in the CC colon and may also play a role in the airway, regulating sodium ion CC absorption and anion secretion. The invention relates to novel disease CC associations of PAR2 polypeptides and polynucleotides. It also relates to CC novel methods of screening for therapeutic agents for the treatment of CC cardiovascular disorders, gastrointestinal and liver diseases, CC neurological disorders, urological disorders, haematological diseases and CC respiratory diseases in a mammal. Suitable therapeutic agents include a CC small molecule, an RNA molecule, an antisense oligonucleotide, a CC polypeptide, an antibody or a ribozyme. The invention also provides CC pharmaceutical compositions for the treatment of diseases and disorders CC associated with PAR2 comprising a PAR2 polypeptide, PAR2 polynucleotide CC or a regulator or modulator of PAR2 activity. Methods of diagnosing these CC diseases and disorders involve determining the amount of PAR2 CC polynucleotide in a sample. XX SQ Sequence 397 AA;			
Query Match	93.7%	Score 1903; DB 8; Length 397;	
Best Local Similarity	96.9%	Pred. No. 2.9e-196;	
Matches 373; Conservative	4;	Mismatches 4; Indels 4; Gaps 1;	

18 SWMTLVPLVSCT----GTTNRSKGRSLIGKVDGTSHVTGKGVTVEVFSVDSPASVLTKG 73


```

Db      13 AIIAASLSCSGTIGTNRSSKGRSLGKVDGSHYTGKVTETVPSVDFASVLTGK 72
Qy      74 LTTVPLPIVVTIVFVVGLPSPNGMALWFLPRTKKGGPAVIYMANLADLLSVIWPPLKI 133
Db      73 LTTVPLPIVVTIVFVVGLPSPNGMALWFLPRTKKGGPAVIYMANLADLLSVIWPPLKI 132
Qy      134 AYHIGNNWLYGBALCNVLI GFPGNNYCSILFMTCISVORVWYVYVPMGHSRKKANIAI 193
Db      133 AYHIGNNWLYGBALCNVLI GFPGNNYCSILFMTCISVORVWYVYVPMGHSRKKANIAI 192
Qy      194 GISLAIWLLILVTIPLPYVVKQTIPIPALNITTCCHDVLPEQLVGMDFNYFLSLAGVFL 253
Db      193 GISLAIWLLILVTIPLPYVVKQTIPIPALNITTCCHDVLPEQLVGMDFNYFLSLAGVFL 252
Qy      254 PPAFLTRASAYVLMIRMLRSSAMDENSEKKRAIKLIVTLAMYLICFTPSNLLLVHYHF 313
Db      253 PPAFLTRASAYVLMIRMLRSSAMDENSEKKRAIKLIVTLAMYLICFTPSNLLLVHYHF 312
Qy      314 LKSGQSHVYALYVALCSTLNSCIDPYYVYFVSHDFRDHAKNALCGRSVTVKQMOV 373
Db      313 LKSGQSHVYALYVALCSTLNSCIDPYYVYFVSHDFRDHAKNALCGRSVTVKQMOV 372
Qy      374 SLTSKGRSKSSSYSSSSTTVKTSY 398
Db      373 SLTSKGRSKSSSYSSSSTTVKTSY 397

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RESULT 9
ADL61221
ID      ADL61221 standard; protein; 397 AA.
XX
XX      ADL61221;
XX
XX      03-JUN-2004 (first entry)
XX
XX      Human coagulation factor II (thrombin) receptor-like 1 protein.
XX
XX      predictor set; protein tyrosine kinase; cytosolic; antiangiogenic;
XX      vasodilator; vasoregulatory; pharmacogenomic; drug sensitivity; breast cancer;
XX      hypervascular disease; angiogenesis; wound healing scar; human;
XX      biomarker; coagulation factor II receptor-like 1; thrombin; receptor.
XX
XX      Homo sapiens.
XX
XX      WO2004020583-A2.
XX
XX      11-MAR-2004.
XX
XX      26-AUG-2003; 2003WO-US026491.
XX
XX      27-AUG-2002; 2002US-0406385P.
XX
XX      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX      Huang F, Han X, Reeves KA, Anler L, Fairchild CR, Lee FY;
XX      Shaw P;
XX
XX      WPI; 2004-239171/22.
XX      N-PSDB; ADL61084.
XX
XX      New predictor sets with a plurality of polymucleotides and/or
XX      polypeptides whose expression pattern predicts cell response to a
XX      compound that modulates protein tyrosine kinase activity, useful in
XX      treating breast cancer.
XX
XX      Claim 9; SEQ ID NO 145; 649pp; English.
XX
XX      The invention relates to a novel predictor set comprising a plurality of
XX      polymucleotides and/or polypeptides whose expression pattern is
XX      predictive of the response of cells to treatment with a compound that
XX      modulates protein tyrosine kinase activity or members of the protein
XX      tyrosine kinase pathway. The molecules of the invention demonstrate

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CC cytosolic, antiangiogenic, vasodilator and vasoregulatory activities and may
 CC be useful in the field of pharmacogenomics, in particular for determining
 CC drug sensitivity and in treating breast cancer, hypervascular disease,
 CC angiogenesis and scars in wound healing. The current sequence is that of
 CC a human protein tyrosine kinase biomarker protein of the invention.

SO Sequence 397 AA;

Query Match 93.54; Score 1898; DB 8; Length 397;
 Best Local Similarity 96.64; Pred. No. 9.9e-196;
 Matches 372; Conservative 5; Mismatches 4; Gaps 1;

```

Qy      18 SVNTLVFLSCT---GTNRSSKGRSLGKVDGSHYTGKVTETVPSVDFASVLTGK 73
Db      13 AIIAASLSCSGTIGTNRSSKGRSLGKVDGSHYTGKVTETVPSVDFASVLTGK 72
Qy      74 LTTVPLPIVVTIVFVVGLPSPNGMALWFLPRTKKGGPAVIYMANLADLLSVIWPPLKI 133
Db      73 LTTVPLPIVVTIVFVVGLPSPNGMALWFLPRTKKGGPAVIYMANLADLLSVIWPPLKI 132
Qy      134 AYHIGNNWLYGBALCNVLI GFPGNNYCSILFMTCISVORVWYVYVPMGHSRKKANIAI 193
Db      133 AYHIGNNWLYGBALCNVLI GFPGNNYCSILFMTCISVORVWYVYVPMGHSRKKANIAI 192
Qy      194 GISLAIWLLILVTIPLPYVVKQTIPIPALNITTCCHDVLPEQLVGMDFNYFLSLAGVFL 253
Db      193 GISLAIWLLILVTIPLPYVVKQTIPIPALNITTCCHDVLPEQLVGMDFNYFLSLAGVFL 252
Qy      254 PPAFLTRASAYVLMIRMLRSSAMDENSEKKRAIKLIVTLAMYLICFTPSNLLLVHYHF 313
Db      253 PPAFLTRASAYVLMIRMLRSSAMDENSEKKRAIKLIVTLAMYLICFTPSNLLLVHYHF 312
Qy      314 LKSGQSHVYALYVALCSTLNSCIDPYYVYFVSHDFRDHAKNALCGRSVTVKQMOV 373
Db      313 LKSGQSHVYALYVALCSTLNSCIDPYYVYFVSHDFRDHAKNALCGRSVTVKQMOV 372
Qy      374 SLTSKGRSKSSSYSSSSTTVKTSY 398
Db      373 SLTSKGRSKSSSYSSSSTTVKTSY 397

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RESULT 10
ABP81907
ID      ABP81907 standard; protein; 397 AA.
XX
XX      ABP81907;
XX
XX      04-MAR-2003 (first entry)
XX
XX      Human proteinase-activated receptor 2 protein SEQ ID NO:300.
XX
XX      G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX      G protein-coupled receptor modulator; antibody; immune-related disease;
XX      growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX      immunological-related cell proliferative disease; autoimmune disease;
XX      Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX      osteoporosis; cardiovascular; inflammation; Crohn's disease; diabetes;
XX      graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX      psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX      mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX      hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX      ulcer.
XX
XX      Homo sapiens.
XX
XX      WO200261087-A2.
XX
XX      08-AUG-2002.
XX
XX      19-DEC-2001; 2001WO-US050107.
XX      19-DEC-2000; 2000US-0257144P.
XX

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RESULT 13

ID ADR46675 standard; protein; 397 AA.

AC ADR46675;

DT 18-NOV-2004 (first entry)

DE Cancer-associated protein, SEQ ID 88.

KM Cytostatic; Gene Therapy; cancer; human.

OS Homo sapiens.

PN MO2004073657-A2.

PD 02-SEP-2004.

PF 19-FEB-2004; 2004MO-US005455.

PR 19-FEB-2003; 2003US-0448784P.

PA (PROT-) PROTEIN DESIGN LABS INC.

PI Aziz N, Gish KC, Wilson KE, Zlocnik A;

DR WPI; 2004-652787/63.

DR N-PSDB; ADR46617.

XX Detecting a pathological cell in a patient for diagnosing or treating
 PT cancer by detecting in a biological sample from the patient genes whose
 PT expression are up-regulated or down-regulated in specific cancers.

PS Claim 1; SEQ ID NO 88; 375pp; English.

XX The present invention relates to a method for detecting cancer in a
 CC patient. The method comprises detecting in a biological sample from the
 CC patient a nucleotide or protein sequence comprising a sequence that is at
 CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
 CC protein sequence (ADR46646-ADR46703). The method is useful for detecting
 CC cancer for preparing a composition for diagnosing or treating cancer.

SQ Sequence 397 AA;

Query Match 93.4%; Score 1897; DB 8; Length 397;

Best Local Similarity 96.6%; Pred. No. 1.3e-195; Matches 372; Conservative 4; Mismatches 5; Indels 4; Gaps 1;

18 SVMTLVFSGT---GTNRSSKGRSLIGKVDGSHYTGKGVETVFSVDEPSASVLTGK 73

13 AILAAASLSCSGTIGTNRSSKGRSLIGKVDGSHYTGKGVETVFSVDEPSASVLTGK 72

74 LTTVFLPIYVTVFVVGLPNSGMAWVFLPRTKKGPAYIVMANLALADLLSVIWPPLKI 133

73 LTTVFLPIYVTVFVVGLPNSGMAWVFLPRTKKGPAYIVMANLALADLLSVIWPPLKI 132

134 AYHIHGNMNYGKALCNVLIGFPYGNMYSILFMTCLSVQRYWVIVNPMGSHSKKANIAI 193

133 AYHIHGNMNYGKALCNVLIGFPYGNMYSILFMTCLSVQRYWVIVNPMGSHSKKANIAI 192

194 GISLAIWLLILVTTIPLYVVKQTIPIPALNITTCDDVLPBOLLVGMFNYFLSLAIGVFL 253

193 GISLAIWLLILVTTIPLYVVKQTIPIPALNITTCDDVLPBOLLVGMFNYFLSLAIGVFL 252

254 FPAFLTASAVVIMIRLRSSAMDENSEKRRKRAIKLIIVTLAMYLICFTPSNLLLVVHYF 313

253 FPAFLTASAVVIMIRLRSSAMDENSEKRRKRAIKLIIVTLAMYLICFTPSNLLLVVHYF 312

314 LHSQGSQSHVYALYIVALCLSTNSCIDPFIYVFSVSHDFPDHAKNLLGSRVFTVQMOV 373

313 LHSQGSQSHVYALYIVALCLSTNSCIDPFIYVFSVSHDFPDHAKNLLGSRVFTVQMOV 372

QY 374 SLTSKGRSSSYSSSTTVKTSY 398
 DB 373 SLTSKGRSSSYSSSTTVKTSY 397

RESULT 14

ID AAR66923 standard; protein; 397 AA.

AC AAR66923;

DT 25-MAR-2003 (revised)

DT 22-AUG-1995 (first entry)

DE Human C140 receptor encoded by cDNA.

KM G-protein-coupled receptor; G-protein; C140 receptor.

OS Homo sapiens.

PN MO9503318-A1.

PD 02-FEB-1995.

PF 26-JUL-1994; 94MO-US008536.

PR 26-JUL-1993; 93US-00097938.

PA (COR-) COR THERAPEUTICS.

PI Scarborough RM, Sundell J;

DR WPI; 1995-075182/10.

DR N-PSDB; AAQ84560.

XX New DNA encoding recombinant C140 receptor - and novel agonists and
 PT antagonists and specific antibodies with therapeutic and diagnostic
 PT applications.

PS Example; Fig 11; 57pp; English.

XX A human intestinal tumour cDNA library was subjected to PCR using primers
 CC designed from the genomic clone (see AAQ84558) and the amplified fragment
 CC was cloned in pSG5 and sequenced. There are four AA differences between
 CC the cDNA encoded sequence and that encoded by the genomic DNA. The
 CC genomic DNA sequence and deduced AA sequence are given in AAQ84560 &
 CC AAR66923. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 397 AA;

Query Match 92.2%; Score 1872; DB 2; Length 397;

Best Local Similarity 95.3%; Pred. No. 6.3e-193; Matches 367; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

18 SVMTLVFSGT---GTNRSSKGRSLIGKVDGSHYTGKGVETVFSVDEPSASVLTGK 73

13 AILAAASLSCSGTIGTNRSSKGRSLIGKVDGSHYTGKGVETVFSVDEPSASVLTGK 72

74 LTTVFLPIYVTVFVVGLPNSGMAWVFLPRTKKGPAYIVMANLALADLLSVIWPPLKI 133

73 LTTVFLPIYVTVFVVGLPNSGMAWVFLPRTKKGPAYIVMANLALADLLSVIWPPLKI 132

134 AYHIHGNMNYGKALCNVLIGFPYGNMYSILFMTCLSVQRYWVIVNPMGSHSKKANIAI 193

133 AYHIHGNMNYGKALCNVLIGFPYGNMYSILFMTCLSVQRYWVIVNPMGSHSKKANIAI 192

194 GISLAIWLLILVTTIPLYVVKQTIPIPALNITTCDDVLPBOLLVGMFNYFLSLAIGVFL 253

193 GISLAIWLLILVTTIPLYVVKQTIPIPALNITTCDDVLPBOLLVGMFNYFLSLAIGVFL 252

254 FPAFLTASAVVIMIRLRSSAMDENSEKRRKRAIKLIIVTLAMYLICFTPSNLLLVVHYF 313

253 FPAFLTASAVVIMIRLRSSAMDENSEKRRKRAIKLIIVTLAMYLICFTPSNLLLVVHYF 312

QY 314 LKSGGSHYALYVALCLSTLNSCIDPFVYVFSHPDPAKALLCRSVRTVKOMOV 373
 DB 313 LKSGGSHYALYVALCLSTLNSCIDPFVYVFSHPDPAKALLCRSVRTVKOMOV 372
 QY 374 SLTSKKSRRKSSSYSSSTTVTKTSY 398
 DB 373 PLTSKKSRRKSSSYSSSTTVTKTSY 397

RESULT 15
 AAM01955
 ID AAM01955 standard; protein; 397 AA.
 AC AAM01955;
 DT 02-APR-1997 (first entry)
 DE Human C140 receptor.
 KM C140 receptor; G-protein linked; coupled; seven pass; agonist;
 KW antagonist; hypertension; hypotension; blood pressure.
 OS Homo sapiens.
 XX
 XX
 FH Key
 FT Peptide
 FT 1..27
 FT /note= "the signal peptide differs from that encoded by a
 FT genomic DNA sequence for this receptor (see AAM01953),
 FT the signal sequence given here is believed to be the
 FT correct sequence"
 FT 28..397
 FT /note= "mature protein"
 XX
 XX
 PN W06323225-A1.
 PD 01-AUG-1996.
 XX
 PD 25-JAN-1996; 96WO-US001179.
 XX
 PR 25-JAN-1995; 95US-00390301.
 XX
 PA (CORP-) COR THERAPEUTICS INC.
 XX
 PI Sundelin J, Scarborough RM;
 XX
 DR WPI, 1996-362813/36.
 DR N-PSDB; AAT32039.
 XX
 PT Vector for expression C140 cell surface receptor in host cell - useful to
 PT identify C140 agonist and antagonists, which are antihypertensives and
 PT elevators of blood pressure, respectively.
 PT
 XX
 PS Example 5; Fig 11A-B; 60pp; English.
 XX
 CC AAM01955 represents the human C140 receptor (C140R). DNA encoding C140R
 CC may be engineered so as to allow the recombinant expression of C140R in a
 CC suitable host cell, i.e. by removing the native expression-control
 CC sequences and replacing them with control sequences operable in the host.
 CC Such a recombinant receptor can be expressed on the surface of oocytes,
 CC this provides a good assay system for identifying agonists/antagonists of
 CC C140R. The C140 receptor is a G-protein linked receptor and a member of
 CC the "seven-pass" transmembrane receptor superfamily (peptide chain of the
 CC receptor passes through the cell membrane seven times, producing seven
 CC transmembrane regions within the receptor molecule). The C140 receptor is
 CC involved in controlling blood pressure. C140 antagonists (see AAM01942-
 CC W01951) are useful to inhibit signalling from this receptor, resulting in
 CC an increase in blood pressure and are therefore useful in pharmaceuticals
 CC for the treatment of hypotension (low blood pressure). Conversely
 CC agonists (see AAM01914-W01941) of C140 are useful in pharmaceuticals for
 CC the treatment of hypertension (high blood pressure)
 CC
 CC Sequence 397 AA,
 SQ

Query Match 92.2%; Score 1872; DB 2; Length 397;
 Best Local Similarity 95.3%; Pred. No. 6,3e-193;
 Matches 367; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

QY 18 SVMTLVFLSCT---GTRSSKGRSLIGKVDGTSHTGKGVTVTFVSVDPSASVLTGK 73
 DB :::::
 DB 13 AILMAASLSCSGRTIGTRSSKGRSLIGKVDGTSHTGKGVTVTFVSVDPSASVLTGK 72
 QY 74 LTTVFLPIVTVTVVAVGLPSNGMALWFLPRTKKGHAVIYMANLADLLSVTFPLKI 133
 DB LTTVFLPIVTVTVVAVGLPSNGMALWFLPRTKKGHAVIYMANLADLLSVTFPLKI 132
 QY 134 AYHIGNNWYIGBALCNVLIGPFYGNMYCSILFWTCLSVORVYVIYVPMGHSRKKANIAI 193
 DB 133 AYHIGNNWYIGBALCNVLIGPFYRNMYCSILFWTCLSVORVYVIYVPMGHSRKKANIAI 192
 QY 194 GISLAIWLLTLVTVIPLYVVKQTIPIPALNITTCDDVLPEQLVGMFNYFLSLAIGVFL 253
 DB 193 GISLAIWLLTLVTVIPLYVVKQTIPIPALNITTCDDVLPEQLVGMFNYFLSLAIGVFL 252
 QY 254 PPAFLTASAYVLMIRMLRSSAMDENSEKKRRAIKIYTVLAWYLICFTSNLLLVHYF 313
 DB 253 PPAFLTASAYVLMIRMLRSSAMDENSEKKRRAIKIYTVLAWYLICFTSNLLLVHYF 312
 QY 314 LKSGGSHYALYVALCLSTLNSCIDPFVYVFSHPDPAKALLCRSVRTVKOMOV 373
 DB 313 LKSGGSHYALYVALCLSTLNSCIDPFVYVFSHPDPAKALLCRSVRTVKOMOV 372
 QY 374 SLTSKKSRRKSSSYSSSTTVTKTSY 398
 DB 373 PLTSKKSRRKSSSYSSSTTVTKTSY 397

Search completed: March 18, 2005, 21:06:43
 Job time : 73.0868 secs

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OM nucleic - nucleic search, using sw model

Run on: March 21, 2005, 12:11:20 / Search time 825.407 Seconds
(without alignments)
10141.072 Million cell updates/sec

Title: US-10-643-627-62

Perfect score: 1414
Sequence: 1 caaagatgtaactacagact.....acaattccacaataaagc 1414

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapept 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: genebegn1980a:*
2: genebegn1990a:*
3: genebegn2000a:*
4: genebegn2001a:*
5: genebegn2001b:*
6: genebegn2002a:*
7: genebegn2002b:*
8: genebegn2003a:*
9: genebegn2003b:*
10: genebegn2003c:*
11: genebegn2003d:*
12: genebegn2004a:*
13: genebegn2004b:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1414	100.0	1414	2	AAQ84560 Human C14
2	1414	100.0	1414	2	AA132039 Human C14
3	1279.4	90.5	2876	12	AD028660 Human PAR
4	1273	90.0	1451	3	AA060319 Human PAR
5	1273	90.0	1451	8	AB242755 Human pro
6	1273	90.0	1451	10	ADK52593 Hematolog
7	1273	90.0	1451	11	ADN39780 Cancer-an
8	1273	90.0	1451	13	ADR46617 Cancer-as
9	1273	90.0	1451	13	ADR74019 Human G-P
10	1263.6	89.4	2848	6	AB235045 Human gen
11	1188.4	84.0	8624	6	AAD44337 Human coa
12	1182.8	83.6	1194	6	AAD44338 Human coa
13	1182.8	83.6	1289	3	AAZ50773 Human pro
14	1179.6	83.4	1194	12	AD029874 Human GPC
15	1105.8	78.2	1255	2	AAQ84558 Human C14
16	1105.8	78.2	1255	2	AA132037 Human C14
17	1055.2	74.6	1068	12	AD128650 Human mod
18	1013.2	71.7	1026	12	AD128651 Human mod
19	951.8	67.3	973	12	AD128652 Human mod
20	833.8	59.0	2713	9	ACC85274 Delayed h

21	833.8	59.0	2732	2	AAQ84559 Murine C1
22	833.8	59.0	2732	2	AA132038 Murine C1
23	829.2	58.6	1200	12	AD030165 Mouse GPC
24	817.8	57.8	1428	10	AB142343 Toxicity
25	805.4	57.0	1477	2	AAQ84557 Murine C1
26	803.8	56.8	1477	2	AA132036 Murine C1
27	383	27.1	486	6	ABK55138 Human col
28	303.2	21.4	493	6	ABK27602 Human col
29	303.2	21.4	641	6	AB137070 Human col
30	166.4	11.8	3418	10	AB141875 Toxicity
31	160.6	11.4	1116	6	ABK70888 Human CDN
32	160.6	11.4	1209	6	ABK70887 Human CDN
33	160.6	11.4	1278	6	ABK70889 Human CDN
34	160.6	11.4	3590	13	ACN38232 Tumour-as
35	156.6	11.1	6203	10	ADG89941 Human coa
36	155.8	11.0	1278	10	ADG89942 Human coa
37	155.8	11.0	1278	12	AD029873 Human GPC
38	155.8	11.0	1764	2	AAQ73590 Fragment
39	155.8	11.0	2910	2	AA162461 Human ade
40	155.8	11.0	3182	3	AA153310 Human ade
41	155.8	11.0	3182	3	AA153310 Human low
42	155.8	11.0	3182	10	AB297126 Human nuc
43	155.8	11.0	3182	11	ABD20975 Human pul
44	155.8	11.0	3299	9	ADA24508 Human CDN
45	155.8	11.0	3472	2	AA232191 Human chr

ALIGNMENTS

RESULT 1	
AAQ84560	AAQ84560 standard; cDNA; 1414 BP.
AAQ84560;	
25-MAR-2003 (revised)	
22-AUG-1995 (first entry)	
Human C140 receptor cDNA.	
G-protein-coupled receptor; G-protein; C140 receptor; ss.	
Homo sapiens.	
Key	Location/Qualifiers
CDS	50..1243
	/*tag= a
W09503318-A1.	
02-FEB-1995.	
26-JUL-1994;	94MO-US008536.
26-JUL-1993;	93US-00097938.
(CORT-) COR THERAPEUTICS.	
Scarborough RM, Sundelin J;	
WPI; 1995-075182/10.	
P-PSDB; AAR66923.	
New DNA encoding recombinant C140 receptor - and novel agonists and	
antagonists and specific antibodies with therapeutic and diagnostic	
applications.	
Claim 1, Fig 11; 57pp; English.	
A human intestinal tumour cDNA library was subjected to PCR using primers	
designed from the genomic clone (see AAQ84558) and the amplified fragment	
was cloned in pSG5 and sequenced. There are four AA differences between	

CC the cDNA encoded sequence and that encoded by the genomic DNA. The
 CC genomic DNA sequence and deduced AA sequence are given in AA084560 &
 CC AAR6923. (Updated on 25-MAR-2003 to correct PN field.)
 XX

Sequence 1414 BP; 335 A; 361 C; 309 G; 409 T; 0 U; 0 Other;

Query Match 100.0%; Score 1414; DB 2; Length 1414;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CAAAGATTGTATAGACTCACTATATAGGCGGAATTCGATCCAGAGAGATGGGAGCCC 60
DB 1 CAAAGATTGTATAGACTCACTATATAGGCGGAATTCGATCCAGAGAGATGGGAGCCC 60
QY 61 CAGCGGCGCTGCTGCTGGGGGCGCCCATCTGCTAGCAGCCCTCTCTCCCTGCAATGG 120
DB 61 CAGCGGCGCTGCTGCTGGGGGCGCCCATCTGCTAGCAGCCCTCTCTCTCCCTGCAATGG 120
QY 121 CACCATCCAGAGAACCAATAGATCTCTTAAAGAGAGAGCCCTTATGTTAGGTTAGTGG 180
DB 121 CACCATCCAGAGAACCAATAGATCTCTTAAAGAGAGAGCCCTTATGTTAGGTTAGTGG 180
QY 181 CACATCCCAAGTCACTGAGAAAAGAGTTACATGTTAAACAGTCTTTTCTGTGATGAGTT 240
DB 181 CACATCCCAAGTCACTGAGAAAAGAGTTACATGTTAAACAGTCTTTTCTGTGATGAGTT 240
QY 241 TTCTGCACTGCTGCTGCTGAGAAAAGTCAACCACTGCTCTTCAATGTTCTACCAAT 300
DB 241 TTCTGCACTGCTGCTGCTGAGAAAAGTCAACCACTGCTCTTCAATGTTCTACCAAT 300
QY 301 TGTGTTTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
DB 301 TGTGTTTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
QY 361 TAAGAAAGAACACCTGCTGCTGATTTACATGAGCCATCTGAGCTTGGCTGACCTCTCTC 420
DB 361 TAAGAAAGAACACCTGCTGCTGATTTACATGAGCCATCTGAGCTTGGCTGACCTCTCTC 420
QY 421 TGTCACTGCTGCTGCTGCTGAGATGCTATCATATACATGAGCAACCTGATTTATGG 480
DB 421 TGTCACTGCTGCTGCTGCTGAGATGCTATCATATACATGAGCAACCTGATTTATGG 480
QY 481 GGAAGCTCTTGTATATGCTTATATGCTTATATGCTTATATGCTTATATGCTTATATG 540
DB 481 GGAAGCTCTTGTATATGCTTATATGCTTATATGCTTATATGCTTATATGCTTATATG 540
QY 541 GTTCAATGACCTGCTGCTGCTGAGATGCTATCATATACATGAGCAACCTGATTTATGG 600
DB 541 GTTCAATGACCTGCTGCTGCTGAGATGCTATCATATACATGAGCAACCTGATTTATGG 600
QY 601 CAGGAAGAGGCAAACTTGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 CAGGAAGAGGCAAACTTGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GGTCAACATCCCTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 GGTCAACATCCCTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 GACCTGTCAATGATGTTTGTGCTGAGCAGCTCTTGGTGGGAGACATGTTCAATTAATCT 780
DB 721 GACCTGTCAATGATGTTTGTGCTGAGCAGCTCTTGGTGGGAGACATGTTCAATTAATCT 780
QY 781 CTCTGTGACCAATTTGGGCTCTTGTCTGTTCCAGGCTTCTTCAAGGCTCTGCTATGAGCT 840
DB 781 CTCTGTGACCAATTTGGGCTCTTGTCTGTTCCAGGCTTCTTCAAGGCTCTGCTATGAGCT 840
QY 841 GATGATCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 GATGATCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 GGCATCAAACTCAATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 GGCATCAAACTCAATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

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QY 961 CCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 CCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 CCTGTACATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 CCTGTACATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 TTACTTGTGTTACATGATTTTACAGGATGATGCAAGAAAGGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 TTACTTGTGTTACATGATTTTACAGGATGATGCAAGAAAGGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 CCGCACTGTAAAGCAGATGCAAGTACCCCTCACTTCAAGAAACACTCCAGAAATCCAG 1200
DB 1141 CCGCACTGTAAAGCAGATGCAAGTACCCCTCACTTCAAGAAACACTCCAGAAATCCAG 1200
QY 1201 CTCTTACTCTTCAAGTTCAACCACTGTTAAAGACCTCTTCAATGATTTTCAAGTCTCAG 1260
DB 1201 CTCTTACTCTTCAAGTTCAACCACTGTTAAAGACCTCTTCAATGATTTTCAAGTCTCAG 1260
QY 1261 ATGGGAATTGCAAGTGAAGATGGAACCTGTTTAAATGTTAAGAGAGAGTGTCTGTATT 1320
DB 1261 ATGGGAATTGCAAGTGAAGATGGAACCTGTTTAAATGTTAAGAGAGAGTGTGTATT 1320
QY 1321 TCCGATCCAGATCTTATTTAAAGCAGAACTGTTTATGCTGCTTAAATGCTTAAAT 1380
DB 1321 TCCGATCCAGATCTTATTTAAAGCAGAACTGTTTATGCTGCTTAAATGCTTAAAT 1380
QY 1381 AAAGCAATGCAATCACAATTTTCAACAATTAAGC 1414
DB 1381 AAAGCAATGCAATCACAATTTTCAACAATTAAGC 1414

```

RESULT 2

AAT32039
 ID AAT32039 standard; cDNA; 1414 BP.

XX AAT32039;

DT 02-APR-1997 (first entry)

XX Human C140 receptor cDNA clone.

XX C140 receptor; G-protein linked; coupled; seven pass; agonist;

KW antagonist; hypertension; hypotension; blood pressure; ss.

XX Homo sapiens.

XX

XX

XX

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XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Key Location/Qualifiers
 CDS 50..1243
 sig_peptide 50..130
 mat_peptide 131..1240
 M09623225-A1.
 01-AUG-1996.
 25-JAN-1996; 96MO-US001179.
 25-JAN-1995; 95US-00390301.
 (COR-) COR THERAPEUTICS INC.
 Sundelin J, Scarborough RM;

XX WPI, 1996-362813/36.
DR P-PSDB, AAW01955.

PT Vector for expression C140 cell surface receptor in host cell - useful to
PT identify C140 agonist and antagonists, which are antihypertensives and
XX elevators of blood pressure, respectively.

PS Example 5, Fig 11A-B, 60pp, English.

XX AAT303 encodes the human C140 receptor (C140R). The sequence may be
XX engineered so as to allow the recombinant expression of C140R in a
XX suitable host cell, i.e. by removing the native expression-control
XX sequence and replacing them with control sequences operable in the host.
XX Such a recombinant receptor can be expressed on the surface of oocytes,
XX this provides a good assay system for identifying agonists/antagonists of
XX the C140 receptor. The C140 receptor is a G-protein linked receptor and a member of
XX the "seven-pass" transmembrane receptor superfamily (peptide chain of the
XX receptor passes through the cell membrane seven times, producing seven
XX transmembrane regions within the receptor molecule). The C140 receptor is
XX involved in controlling blood pressure. C140 antagonists (see AAW01942-
XX W01951) are useful to inhibit signalling from this receptor, resulting in
XX an increase in blood pressure and are therefore useful in pharmaceuticals
XX for the treatment of hypertension (low blood pressure). Conversely
XX agonists (see AAW01914- AAW01941) of C140 are useful in pharmaceuticals
XX for the treatment of hypertension (high blood pressure).

SO Sequence 1414 BP, 335 A, 361 C, 309 G, 409 T, 0 U, 0 Other;

Query Match 100.0%; Score 1414; DB 2; Length 1414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGAATTGTAATGAGTCACTATGAGCGGAATTGATCCAGAGATGCGAGCCC 60
DB 1 CAAGAATTGTAATGAGTCACTATGAGCGGAATTGATCCAGAGATGCGAGCCC 60
QY CAGCGGCGGCTGCTGCTGCGGCGCGCATCTGCTAGCAGCCCTCTCTCGCAGTGG 120
DB CAGCGGCGGCTGCTGCTGCGGCGCGCATCTGCTAGCAGCCCTCTCTCGCAGTGG 120
QY 61 CAGCGGCGGCTGCTGCTGCGGCGCGCATCTGCTAGCAGCCCTCTCTCGCAGTGG 120
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QY 181 CACATCCCACTGACATGAGAAAGAGATTACAGTTGAAACAGTCTTTCTGTGATGATT 240
DB 181 CACATCCCACTGACATGAGAAAGAGATTACAGTTGAAACAGTCTTTCTGTGATGATT 240
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DB 361 TAAAGAAAGACACCTGCTGTGATTTACATGCGCAATCTGCGCTTGTGATGCTCTCTC 420
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DB 421 TGTGATCTGTGCTGCTGCGGAAAGTTCATACATACATGCGCAACATGGAATTAATGG 480
QY 481 GGAAGCTCTTGTGATATGCTTAATGGCTTTTCTATCGCAATGATCTTCAATTC 540
DB 481 GGAAGCTCTTGTGATATGCTTAATGGCTTTTCTATCGCAATGATCTTCAATTC 540
QY 541 CTTGATGACCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 541 CTTGATGACCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600

QY 601 CAGAGAAAGAGCAAAATTCGCAATGCGATCTCCCTGGCAATATGCTGCTGCT 660
DB 601 CAGAGAAAGAGCAAAATTCGCAATGCGATCTCCCTGGCAATATGCTGCTGCT 660
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DB 661 GGTACCAATCCCTTTGTATGCTGTAAGCAGACCAATCTTCAATCTGCTGCTGCTGCT 720
QY 721 GACCTGCAATGATGTTTGTGCTGTAAGCAGACCAATCTTCAATCTGCTGCTGCTGCT 780
DB 721 GACCTGCAATGATGTTTGTGCTGTAAGCAGACCAATCTTCAATCTGCTGCTGCTGCT 780
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DB 781 CTTCTGCGCAATGAGGCTCTTCTGTTCCAGGCTCTTCAAGGCTCTGCTGCTGCTGCT 840
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DB 841 GATGATCAGAAATGCTGCAATCTTCTGCTGCAATGATGATGATGATGATGATGATGAT 900
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QY 1321 TCCGATCCAGATCTTAATTAAGCAGATGTTTATGAGCTTAATTAATGTTACAAAT 1380
DB 1321 TCCGATCCAGATCTTAATTAAGCAGATGTTTATGAGCTTAATTAATGTTACAAAT 1380
QY 1381 AAAGCAATGATCACAATTTCACAATTAAGC 1414
DB 1381 AAAGCAATGATCACAATTTCACAATTAAGC 1414

RESULT 3

ADO28600
ID ADO28600 standard; cDNA; 2876 BP.

XX ADO28600;

XX 12-AUG-2004 (first entry)

XX Human PAR2 encoding cDNA SEQ ID NO:29.

XX high-grade dysplasia; HGD; oesophageal adenocarcinoma;

XX neo-plastic transformation; cancer; cytotoxic; gene therapy; human;

XX PAR2; chromosome 5; gene; ss.

XX Homo sapiens.

```

FH Key Location/Qualifiers
FT CDS 158..1348
FT /tag= a
FT /product= "PAR2"
FT /transl_except= (pos:287..292,aa:Ser)
FT /transl_except= (pos:461..466,aa:Thr)
FT /transl_except= (pos:635..640,aa:Ser)
FT /transl_except= (pos:809..814,aa:Ala)
FT /transl_except= (pos:983..988,aa:Ser)
FT /transl_except= (pos:1157..1162,aa:Asn)
FT /transl_except= (pos:1331..1336,aa:Lys)
PN MO200404178-A2.
PD 27-MAY-2004.
XX
XX
XX 13-NOV-2003; 2003MO-US036260.
XX
XX 13-NOV-2002; 2002US-0425813P.
XX (GETH ) GENENTECH INC.
XX
XX Smith V;
XX
XX WPI, 2004-420319/39.
XX P-PSDB; ADO28601.
XX
XX Detecting of high-grade dysplasia in cells of a mammalian tissue sample
XX comprises establishing the level of expression in the test tissue sample
XX of the gene.
XX
XX Claim 1; SEQ ID NO 29; 256bp; English.
XX
XX The present invention describes a method for detecting high-grade
XX dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
XX (1) identifying an oesophageal tissue susceptible to oesophageal
XX adenocarcinoma; (2) determining the predisposition of a mammalian tissue
XX to a neo-plastic transformation by detecting HGD in cells of the tissue;
XX and (3) detecting cancer in a patient. The method can be used in
XX detecting HGD and cancer in cells of a mammalian tissue sample. The
XX methods and compositions of the present invention can be used in treating
XX and preventing HGD and cancer, and in gene therapy. The present sequence
XX encodes human PAR2, which is used in the exemplification of the present
XX invention. The human PAR2 gene is located on chromosome 5.
XX
SQ Sequence 2876 BP; 772 A; 632 C; 629 G; 843 T; 0 U; 0 Other;
Query Match 90.5%; Score 1279.4; DB 12; Length 2876;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1298; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 29 GGCGAATTGGGATTCAGAGAGATGCGAGGCGGCGGCGTGGCTGGGGGCGGC 88
DB 134 GGCGTGGGGCTTCAGAGAGATGCGAGGCGGCGGCGGCGTGGCTGGGGGCGGC 193
QY 89 ATCTCTGACGACGCTCTCTCTCTGCACTGAGGCAATCCAGAAACAATAGTCTCT 148
DB 194 ATCTCTGACGACGCTCTCTCTCTGCACTGAGGCAATCCAGAAACAATAGTCTCT 253
QY 149 AAAGGAAGAGCTTATTTGTAAGTGAATGAGCAATCCCACTCATGGAAGAGATT 208
DB 254 AAAGGAAGAGCTTATTTGTAAGTGAATGAGCAATCCCACTCATGGAAGAGATT 313
QY 209 ACAGTTGAACAGTCTTTCTGAGATGAGTTTCTGCACTCTGCTGCTGGAAGATG 268
DB 314 ACAGTTGAACAGTCTTTCTGAGATGAGTTTCTGCACTCTGCTGCTGGAAGATG 373
QY 269 ACCACTGTCTTCTTCCATTTGTCTACACAAATGTTTGCGGTGGGTTTCCAGTAAC 328
DB 374 ACCACTGTCTTCTTCCATTTGTCTACACAAATGTTTGCGGTGGGTTTCCAGTAAC 433
QY 329 GGCGATGGCCCTTATGGGCTTTTCTTCCGAACCTAAGAAAGACCTGTGTGATTTAC 388

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DB 434 GGCGATGGCCCTTATGGGCTTTTCTTCCGAACCTAAGAAAGACCTGTGTGATTTAC 493
QY 389 ATGGCCCAATGTGGCTTGGCTGACCTCTCTGTGATCTGAGTCCCTTGAAGATGGC 448
DB 494 ATGGCCCAATGTGGCTTGGCTGACCTCTCTGTGATCTGAGTCCCTTGAAGATGGC 553
QY 449 TATCAGATTCATGCGCAACACTGAGATTTATGGGAAAGCTCTTTGTAATGTCTTATGGC 508
DB 554 TATCAGATTCATGCGCAACACTGAGATTTATGGGAAAGCTCTTTGTAATGTCTTATGGC 613
QY 509 TTTTCTTATGCGAACAATGACTGTTCCATTCTCTTCATGACCTGCTCAGTGTGAGAG 568
DB 614 TTTTCTTATGCGAACAATGACTGTTCCATTCTCTTCATGACCTGCTCAGTGTGAGAG 673
QY 569 TATTTGGTATCGTGAACCCCAATGGGCACTCCAGGAAGAGCAAACTTGCATTTGGC 628
DB 674 TATTTGGTATCGTGAACCCCAATGGGCACTCCAGGAAGAGCAAACTTGCATTTGGC 733
QY 629 ATCTCCCTGGCAATATGGCTGCTGACTGCTGTGTCACATCCCTTTGTAATGTCTGAAG 688
DB 734 ATCTCCCTGGCAATATGGCTGCTGACTGCTGTGTCACATCCCTTTGTAATGTCTGAAG 793
QY 689 CAGACCATCTTGAATTCCTGGCCGCTGAACATCAGACCTGTGATGATTTTGCTGAGAG 748
DB 794 CAGACCATCTTGAATTCCTGGCCGCTGAACATCAGACCTGTGATGATTTTGCTGAGAG 853
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DB 974 ATGATGAAAGCACTCAGAGAAAGAAAGAGAGGCAATCAATCTGATTCATCTGCTG 1033
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DB 1154 ACCCTTAACAGCTGATGACACCTTTTGTCTAATTAATTTGTTTCAATGATTTACAGGAT 1213
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DB 1214 CATGCAAGAAAGCTCTCTCTTTCGGAAGTGTCCGCACTGTAAAGAGATGCAAGTACC 1273
QY 1169 CTCACCTCAAGAAAGCACTCCAGAAATCAGCTCTTACTCTTCAAGTTCAACACTGTT 1228
DB 1274 CTCACCTCAAGAAAGCACTCCAGAAATCAGCTCTTACTCTTCAAGTTCAACACTGTT 1333
QY 1229 AAGACCTCTATTTGATTTTTCAGGTCCTCAGATGGAAATTCACAGATGAGATGGAAC 1288
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DB 1394 CTGTTTAATGTTATGAGACGCTGTCTGTTATTTCCGATTCAGATCTTAATTAAGCAGAA 1453
QY 1349 CTGTTTAT 1357
DB 1454 CATGTGAT 1462

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RESULT 4
AAC60319

ID	Accession	Standard	DNA	1451	BP.
XX	AC	AA60319			
XX	AC	AA60319			
XX	DT	19-FEB-2001	(first entry)		
XX	DE	Human PAR-2 DNA.			
XX	XX				
XX	OS	Homo sapiens.			
XX	XX	WO200063371-A1.			
XX	PD	26-OCT-2000.			
XX	PP	17-APR-2000; 2000WO-GB001455.			
XX	PR	15-APR-1999; 99GB-00008513.			
XX	PA	(UYSO-) UNIV SOUTHAMPTON.			
XX	PI	Walls AF, Palmer K, Compton SJ, Cairns JA, Gough AC;			
XX	DR	WPI, 2000-679599/66.			
XX	PT	Protease activated receptor 2 variance useful for treating inflammatory			
XX	PT	diseases such as asthma, arthritis and psoriasis, and as hypertensives,			
XX	PT	has reduced sensitivity to trypsin.			
XX	XX	Disclosure; Page 54-55; 59pp; English.			
XX	PS				
XX	CC	The present invention relates to a variant protease activated receptor 2			
XX	CC	(PAR-2). The invention is useful for identifying an individual having a			
XX	CC	polymorphism in the ECL-2 region of one or both PAR-2 gene alleles. The			
XX	CC	invention may be used to develop treatments for inflammatory diseases			
XX	CC	such as asthma, chronic obstructive pulmonary diseases, arthritis,			
XX	CC	inflammatory bowel diseases, psoriasis and eczema, multiple sclerosis and			
XX	CC	to raise blood pressure			
XX	XX				
XX	XX	Sequence 1451 BP, 310 A, 389 C, 346 G, 406 T, 0 U, 0 Other;			
XX	XX				
XX	XX	Query Match 90.0%; Score 1273; DB 3; Length 1451;			
XX	XX	Best Local Similarity 97.7%; Pred. No. 0;			
XX	XX	Matches 1291, Conservative 0; Mismatches 30; Indels 0; Gaps 0			
XX	QY	29 GCGCAATTCGATCCAGAGATCGAGAGCCGACGCGCGCTGCTGGGGCGCCG 88			
XX	DB	127 GCGCTCGGGGCTTCCAGGAGATGCGGAGCCGACGCGCGCTGCTGGGGCGCCG 186			
XX	QY	89 ATCCGCTAGACGAGCTCTCTCCGCGAGTGGGACATCCAGGAACCAATGATCTCT 148			
XX	DB	187 ATCCGCTAGACGAGCTCTCTCTCCGCGAGTGGGACATCCAGGAACCAATGATCTCT 246			
XX	QY	149 AAAGAGAGAGGCTTATGTTGTAAGTTGATGACATCCGACGTCACTGGAAAAGATT 208			
XX	DB	247 AAAGAGAGAGGCTTATGTTGTAAGTTGATGACATCCGACGTCACTGGAAAAGATT 306			
XX	QY	209 ACAGTTGAAACAGTCTTTTCTGTGATGATGTTTCTGCATCTGCTCGTGGAAAAGTTG 268			
XX	DB	307 ACAGTTGAAACAGTCTTTTCTGTGATGATGTTTCTGCATCTGCTCGTGGAAAAGTTG 366			
XX	QY	269 ACCACTGTCTTCTTCAATGTCATCAACAATGTTGTTGGGTGGTTGGCAAGTAC 328			
XX	DB	367 ACCACTGTCTTCTTCAATGTCATCAACAATGTTGTTGGGTGGTTGGCAAGTAC 426			
XX	QY	329 GGCAATGAGCCCTATGGGCTTTCTTTTCCGAACTAAGAGAGACACCTGCTGATTAC 388			
XX	DB	427 GGCAATGAGCCCTATGGGCTTTCTTTTCCGAACTAAGAGAGACACCTGCTGATTAC 486			
XX	QY	389 ATGGCAATTCGGGCTTGGCTGACCTCTCTGTGATCTGGTTCCCTTGAAGATTGCC 448			

Db	487	ATGGCGAATCTGGCCTTGGCTGACCTCCTCTCTGCACTTGGTTCCCTTGAAAGTTGGC	546
Qy	449	TATCACATACATGGCAACAACCTGATTTATGGGAAAGCTCTTTGTATATGTGCTTATTTGGC	508
Db	547	TATCACATACATGGCAACAACCTGATTTATGGGAAAGCTCTTTGTATATGTGCTTATTTGGC	606
Qy	509	TTTTTCTATCCGAACATGTACTGTGTTCCATTTCTCTTCAATGACCTGGCTCAGATGTGAGAG	568
Db	607	TTTTTCTATGGCAACATGTACTGTTCATTTCTCTTCAATGACCTGGCTCAGATGTGAGAG	666
Qy	569	TATTGGGTCATGTGAAACCCCATGGGGCACTCCAGAGAAAGAGGCAAACTTGGCAATTGGC	628
Db	667	TATTGGGTCATGTGAAACCCCATGGGGCACTCCAGAGAAAGAGGCAAACTTGGCAATTGGC	726
Qy	629	ATCTCCCTGGCAATATGGCTGTGCTGACTGTGCTGTGTACCATCCCTTGTATGTGTGAAG	688
Db	727	ATCTCCCTGGCAATATGGCTGTGCTGACTGTGCTGTGTACCATCCCTTGTATGTGTGAAG	786
Qy	689	CAGACCATCTTCAATCTCTGCTCCCTGAACATCAAGACCTGTCAATGATGTTTGGCTGAGAG	748
Db	787	CAGACCATCTTCAATCTCTGCTCCCTGAACATCAAGACCTGTCAATGATGTTTGGCTGAGAG	846
Qy	749	CTCTTGGTGGAGACATGTGCAATTACTTCCTCTCTGGGCAATGGGGTCTTTCCTGTC	808
Db	847	CTCTTGGTGGAGACATGTGCAATTACTTCCTCTCTGGGCAATGGGGTCTTTCCTGTC	906
Qy	809	CCAGCCTTCTCAACAGCCTCTGCTGCTGATGTGATCAGATGCTGCGATCTTCTGACC	868
Db	907	CCAGCCTTCTCAACAGCCTCTGCTGCTGATGTGATCAGATGCTGCGATCTTCTGACC	966
Qy	869	ATGATGAAAACTCAGAGAGAAAAAGAAAGGGGCATCAAACTCATTTGTCACTGTCTGTG	928
Db	967	ATGATGAAAACTCAGAGAGAAAAAGAAAGGGGCATCAAACTCATTTGTCACTGTCTGTG	1026
Qy	929	GGCAGTATACCGATCTGTCACTCCCTATGTAACCTGTGCTTGTGAGGACATTAATTTCTG	988
Db	1027	GGCAGTATACCGATCTGTCACTCCCTATGTAACCTGTGCTTGTGAGGACATTAATTTCTG	1086
Qy	989	ATTAAAGCCAGGGCCAGAGCCATGTCTATGACCCTGTGACATTTGATGACCCTGTGCTCT	1048
Db	1087	ATTAAAGCCAGGGCCAGAGCCATGTCTATGACCCTGTGACATTTGATGACCCTGTGCTCT	1146
Qy	1049	ACCCTTAAACAGCTGATGACACCCCTTGTCTAATTACTTGTGTTTCAATGATTTCAAGGAT	1106
Db	1147	ACCCTTAAACAGCTGATGACACCCCTTGTCTAATTACTTGTGTTTCAATGATTTCAAGGAT	1206
Qy	1109	CATCGAAGAAGCGCTCTCTTGTGCGAAGTCCGCACTGTAAAGCAGATGCAAGTACCC	1168
Db	1207	CATCGAAGAAGCGCTCTCTTGTGCGAAGTCCGCACTGTAAAGCAGATGCAAGTACCC	1266
Qy	1169	CTCAACCTCAAGAAACACTCCAGGAAATCCAGCTCTTAATCTTCAAGTTCAACCACTGTT	1228
Db	1267	CTCAACCTCAAGAAACACTCCAGGAAATCCAGCTCTTAATCTTCAAGTTCAACCACTGTT	1326
Qy	1229	AAGACCTTCTATATGAGTTTCCAGGTCTCAGATGGAAATTGCAACATGAGATGTGAAC	1288
Db	1327	AAGACCTTCTATATGAGTTTCCAGGTCTCAGATGGAAATTGCAACATGAGATGTGAAC	1386
Qy	1289	CTGTTTAATGTTAATGAGACGTGTCTGTATATTTCCGATCCAGATCTTAAATTAAGCAAAA	1348
Db	1387	CTGTTTAATGTTAATGAGACGTGTCTGTATATTTCTTAATCAAAAAGGTCTCACACATAC	1446
Qy	1349	C 1349	
Db	1447	C 1447	

XX 04-MAR-2003 (first entry)
 DT Human proteinase-activated receptor 2 nucleotide seq ID NO:299.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related disease; cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiovascular; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; db.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burnier GC, Roush CL, Brown JP;
 XX
 DR WPI; 2003-046718/04.
 XX
 PT P-PSDB; ABP81907.
 PT
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 PT
 PS Disclosure; Fig 1; 523dp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnoses. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 1451 BP; 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other;

Query Match 90.0%; Score 1273; DB 8; Length 1451;
 Best local Similarity 97.7%; Pred. No. 0;
 Matches 1291; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY	29	GGCGAATTGGATCCAGAGGATGCGGAGCCCCAGCGCGGCTGCTGGGGCGCGCC	88
DB	127	GGCGTGGGGCTTCCAGAGAGTGGAGCCCCAGCGCGGCTGCTGGGGCGCGCC	186
QY	89	ATCTGCTAGGAGCCCTCTCTCTGACGTGACCAATCCAGAAACAATGATCTCT	148
DB	187	ATCTGCTAGGAGCCCTCTCTCTGACGTGACCAATCCAGAAACAATGATCTCT	246
QY	149	AAAGAGAGAGCCCTTATGTTAGGTTGATGACATCCACGTCATGAGAAAGAGTT	208
DB	247	AAAGAGAGAGCCCTTATGTTAGGTTGATGACATCCACGTCATGAGAAAGAGTT	306
QY	209	ACAGTTGAAACAGCTTTTCTGTGATGATGATTTCTGATCTGTCTCGTGAAGAACTG	268
DB	307	ACAGTTGAAACAGCTTTTCTGTGATGATGATTTCTGATCTGTCTCGTGAAGAACTG	366
QY	269	ACCAGTCTTCTCTTCCAAATGTTGTTACAAATTTGATGATGATGATGATGATGAT	328
DB	367	ACCAGTCTTCTCTTCCAAATGTTGTTACAAATTTGATGATGATGATGATGATGAT	426
QY	329	GGCATGGCCCTATGAGTCTTTCTTTCCGAACCTAAGAGAGCACTGCTGATTTAC	388
DB	427	GGCATGGCCCTATGAGTCTTTCTTTCCGAACCTAAGAGAGCACTGCTGATTTAC	486
QY	389	ATGGCCAACTGCGCTTGGCTGACCTCTCTCTGTCATCTGTTCCCTTGAAGATTGCG	448
DB	487	ATGGCCAACTGCGCTTGGCTGACCTCTCTCTGTCATCTGTTCCCTTGAAGATTGCG	546
QY	449	TATCATATCATGAGCAACAATGATTTATGAGGAAAGCTTTGTAATGCTTTATGAGC	508
DB	547	TATCATATCATGAGCAACAATGATTTATGAGGAAAGCTTTGTAATGCTTTATGAGC	606
QY	509	TTTTTCTATGGAACATGATCTGTTCCATTTCTTTATGATGATGATGATGATGATG	568
DB	607	TTTTTCTATGGAACATGATCTGTTCCATTTCTTTATGATGATGATGATGATGATG	666
QY	569	TATTTGGTATGATGAAACCCCATGAGGCACTCCAGAAAGAAAGCAATTCCTATGAGC	628
DB	667	TATTTGGTATGATGAAACCCCATGAGGCACTCCAGAAAGAAAGCAATTCCTATGAGC	726
QY	629	ATCTCCCTGGAATATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	688
DB	727	ATCTCCCTGGAATATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	786
QY	689	CAGACCATCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	748
DB	787	CAGACCATCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	846
QY	749	CTCTTGTGTGAGACATGTTCAATTACTTCTCTCTGCGCAATGAGGCTCTTCTGTTT	808
DB	847	CTCTTGTGTGAGACATGTTCAATTACTTCTCTCTGCGCAATGAGGCTCTTCTGTTT	906
QY	809	CCAGCTTCTCTCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	868
DB	907	CCAGCTTCTCTCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	966
QY	869	ATGATGAAACTCAGAGAAAGAAAGAAAGAGGCGCATCAATTCATTCATCTGCTG	928
DB	967	ATGATGAAACTCAGAGAAAGAAAGAAAGAGGCGCATCAATTCATTCATCTGCTG	1026
QY	929	GGCATGTACTGATCTGCTTCACTCTGATTAACCTTGTGCTGTGTGATATTTTCTG	988
DB	1027	GGCATGTACTGATCTGCTTCACTCTGATTAACCTTGTGCTGTGTGATATTTTCTG	1086
QY	989	ATTTAGAGCCAGAGGCGAGAGCCATGTTATGCTGCTGATCATTTGAGCCCTGCTCT	1048
DB	1087	ATTTAGAGCCAGAGGCGAGAGCCATGTTATGCTGCTGATCATTTGAGCCCTGCTCT	1146
QY	1049	ACCTTTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1108
DB	1147	ACCTTTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1206
QY	1109	CATGCAAGAACGCTCTCTCTTGTCCGAAGTGTCCGACATGTTAAGCAAGATGACAT	1168

Db 1207 CATGCAAGAAAGCTCTCTCTTTCGGAAGTCCGCACTGTAAGCAAGATATCC 1266
 Qy 1169 CTCACCTCAAGAAACCTCCAGGAATCCAGCTCTTAATCTTCAAGTTCAACCACTGTT 1228
 Db 1267 CTCACCTCAAGAAACCTCCAGGAATCCAGCTCTTAATCTTCAAGTTCAACCACTGTT 1326
 Qy 1229 AAGACCTCTTATAGTTTTCAGATCTCCAGATGGGAATGCAAGTGAATGGAAC 1288
 Db 1327 AAGACCTCTTATAGTTTTCAGATCTCCAGATGGGAATGCAAGTGAATGGAAC 1386
 Qy 1289 CTGTTTATGTTATGAGACCTGCTCTGTTATTTCCGATCCAGATCTTATTTAAAGCAAA 1348
 Db 1387 CTGTTTATGTTATGAGACCTGCTCTGTTATTTCCGATCCAGATCTTATTTAAAGCAAA 1446
 Qy 1349 C 1349
 Db 1447 C 1447

RESULT 6
ADKS2593

ID ADKS2593 standard; DNA; 1451 BP.

AC ADKS2593;

DT 06-MAY-2004 (first entry)

DE Hematological disorder associated Gene ID 340.

XX cytostatic; antineoplastic; anti-sickling; virucide; hemostatic; nephrotropic;
 KM cytostatic; thrombolytic; antiparasitic; gene therapy;
 KM hematologic disorder; cancer; Sickle Cell Anemia;
 KM Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;
 KM Reticuloblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;
 KM transfusion reaction; Erythroblastosis; mechanical trauma;
 KM micro-angiopathic hemolytic anemia; parasite infection; gene; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 148..1341

FT /*tag= a

PN NC02003065871-A2.

PD 14-AUG-2003.

PF 28-JAN-2003; 2003W0-US002484.

PR 04-FEB-2002; 2002US-0354333P.

PR 28-FEB-2002; 2002US-0360258P.

PR 15-MAR-2002; 2002US-0364476P.

PR 26-APR-2002; 2002US-0375626P.

PR 06-JUN-2002; 2002US-0386494P.

PR 24-JUN-2002; 2002US-0390965P.

PR 28-JUN-2002; 2002US-0392480P.

PR 03-JUL-2002; 2002US-0394128P.

PR 31-JUL-2002; 2002US-0399783P.

PR 13-AUG-2002; 2002US-0403221P.

PR 30-AUG-2002; 2002US-0407045P.

PR 25-NOV-2002; 2002US-0429048P.

(MILL-) MILLENNIUM PHARM INC.

PI Carrol JM, Healy A, Welch NS, Kelly LM;

DR WPI; 2003-731464/69.

DR P-PSDB; ADKS2594.

XX Identifying a compound capable of treating a hematologic disorder (e.g.
 PT anemia or leukemia) comprises assaying the ability of the compound to
 PT modulate the expression or activity of e.g. 131,148, 199 or 12303

PT polypeptide or nucleic acid.

XX Disclosure; SEQ ID NO 51; 232bp; English.

XX The invention relates to a method of identifying a compound capable of
 CC treating a hematologic disorder comprises assaying the ability of the
 CC compound to modulate 131,148, 199, 12303, 13906, 15513, 17822, 302, 5677,
 CC 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871,
 CC 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic
 CC acid expression or polypeptide activity, thus, identifying a compound
 CC capable of treating a hematologic disorder. The methods are useful in
 CC diagnosing, preventing and treating hematological disorders, such as
 CC cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia,
 CC Polycythemia Vera, Lymphoma, Reticuloblastoma, Hemophilia, disorders
 CC associated with an increased risk of thrombosis, Herpes, Thalassemia,
 CC antibody-mediated disorders such as transfusion reactions and
 CC Erythroblastosis, mechanical trauma to red blood cells such as micro-
 CC angiopathic hemolytic anemias, infections by parasites or chemical
 CC injuries. The methods may also be used for identifying compounds that
 CC modulate hematological disorders. This sequence corresponds to one of the
 CC genes modulated the compound.

XX Sequence 1451 BP; 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other;

SQ Query Match 90.0%; Score 1273; DB 10; Length 1451;

XX Best Local Similarity 97.7%; Pred. No. 0;

XX Matches 1291; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 29 GGCAGATTCGATTCAGAGAGATGCGAGCCCGAGCGGCGTGGCTGGGGCCGCC 88
 Db 127 GGGGTGGGGCTTCCAGAGAGATGCGAGCCCGAGCGGCGTGGCTGGGGCCGCC 186
 Qy 89 ATCTGTACACAGCTCTCTCTCTGATGAGGACCATCCAAAGCAATTAATCTCT 148
 Db 187 ATCTGTACACAGCTCTCTCTCTGATGAGGACCATCCAAAGCAATTAATCTCT 246
 Qy 149 AAGAGAGAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 208
 Db 247 AAGAGAGAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 306
 Qy 209 ACAATTGAAACAGTCTTTTCTGATGATGATGATGATGATGATGATGATGATGAT 268
 Db 307 ACAATTGAAACAGTCTTTTCTGATGATGATGATGATGATGATGATGATGATGAT 366
 Qy 269 ACCACTGCT 328
 Db 367 ACCACTGCT 426
 Qy 329 GGCATGCGCTATGAGGCTTCTCTTCCGAACTAAGAGAGAGAGAGAGAGAGAGAG 388
 Db 427 GGCATGCGCTATGAGGCTTCTCTTCCGAACTAAGAGAGAGAGAGAGAGAGAGAG 486
 Qy 389 ATGGCAATGAGCGCTTGGCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 448
 Db 487 ATGGCAATGAGCGCTTGGCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 546
 Qy 449 TATCACTATATGAGCAACATGATTTATGAGGAGAGAGAGAGAGAGAGAGAGAG 508
 Db 547 TATCACTATATGAGCAACATGATTTATGAGGAGAGAGAGAGAGAGAGAGAGAG 606
 Qy 509 TTTTCTATGAGCAACATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 568
 Db 607 TTTTCTATGAGCAACATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 666
 Qy 569 TATGGGTATGAGCAACATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 628
 Db 667 TATGGGTATGAGCAACATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
 Qy 629 ATCTCTGAGCAATATGAGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 688
 Db 727 ATCTCTGAGCAATATGAGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 746
 Qy 689 CAGACATCTTCAATCTGCGCTGAGACATCAGACAGCTGATGATGATGATGATGAT 748

Db	787	CAGACCACTCTTCATTCTTCGCCCCCTGAAACATCAAGACCTTCATGATGTTTTCCTBAGCAG	846
Qy	749	CTCTTGATGGAGACATGTTCAATTACTTCTCTCTCTGAGCAATYGGGGTCTTTCGTTC	808
Db	847	CTCTTGATGGAGACATGTTCAATTACTTCTCTCTCTGAGCAATYGGGGTCTTTCGTTC	906
Qy	809	CCAGCCTTCTCTCAACGCTCTGCGCTATGTGCTGATGATCAGAAATGCTGCCATCTTCTGCC	868
Db	907	CCAGCCTTCTCTCAACGCTCTGCGCTATGTGCTGATGATCAGAAATGCTGCCATCTTCTGCC	966
Qy	869	ATGATGAAAACTCAGAGAAAAAGAAAGAGAGGGCCATCAACTATTTGCACTGTCCTG	928
Db	967	ATGATGAAAACTCAGAGAAAAAGAAAGAGGGCCATCAACTATTTGCACTGTCCTG	1026
Qy	929	GGCATGTACCTGATCTGCTTCACTCTTAGTAACTTCTGCTTGATGATCAATATTTCTG	988
Db	1027	GCCATGTACCTGATCTGCTTCACTCTTAGTAACTTCTGCTTGATGATCAATATTTCTG	1086
Qy	989	ATTAAAGAGCCAGGGCCAGAGCCATGTCTATGCTCTGTACATTGTAGCCCTCTGCTCTCT	1048
Db	1087	ATTAAAGAGCCAGGGCCAGAGCCATGTCTATGCTCTGTACATTGTAGCCCTCTGCTCTCT	1146
Qy	1049	ACCCTTAAACAGCTGATGAGACCCCTTGCTTAACTTCTTGTTTCAATGATTTACAGGGAT	1108
Db	1147	ACCCTTAAACAGCTGATGAGACCCCTTGCTTAACTTCTTGTTTCAATGATTTACAGGGAT	1206
Qy	1109	CATGCAAGAAAGACGCTCTCTCTTGGCGAAGTGTCCGCACTGTAAAGCAGATGCAAGTACC	1168
Db	1207	CATGCAAGAAAGACGCTCTCTCTTGGCGAAGTGTCCGCACTGTAAAGCAGATGCAAGTACC	1266
Qy	1169	CTCACCTTCAAGAAACACTCCAGGAATCCAGCTCTTACTCTTCAAGTTCAACCACTGTT	1228
Db	1267	CTCACCTTCAAGAAACACTCCAGGAATCCAGCTCTTACTCTTCAAGTTCAACCACTGTT	1326
Qy	1229	AAGACCTTCTTATGATGTTTCCAGGTCCTCCAGATGGGAAATTGCACAGTAGGATGTGAAAC	1288
Db	1327	AAGACCTTCTTATGATGTTTCCAGGTCCTCCAGATGGGAAATTGCACAGTAGGATGTGAAAC	1386
Qy	1289	CTGTTTAAATGTTATGAGGACGTGTCGTATTATTTCCGATCCAGATCTTATTAAAGCAGAA	1348
Db	1387	CTGTTTAAATGTTATGAGGACGTGTCGTATTATTTCCGATCCAGATCTTATTAAAGCAGAA	1446
Qy	1349	C 1349	
Db	1447	C 1447	
RESULT 7			
ADN39780			
ID	ADN39780	standard; cDNA; 1451 BP.	
AC	ADN39780;		
XX	17-JUN-2004	(first entry)	
XX			
DE	Cancer/angiogenesis/fibrosis-related nucleic acid, SBO ID NO:C152.		
XX			
KW	Human; differential expression; cancer; angiogenic disorder;		
KW	fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;		
KW	inflammatory disease; autoimmune disease;		
KW	retinal neovascularisation syndrome; scarring; uterine fibroid;		
KW	detection; diagnosis; prognosis; drug screening; drug targeting;		
KW	wound healing; contraception; cytostatic; cardiant; immunomodulatory;		
KW	vulneraty; gene therapy; vaccine; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003042661-A2.		
XX			
PD	22-MAY-2003.		
XX			
PF	13-NOV-2002; 2002WO-US036810.		

XX	13-NOV-2001;	2001US-0350666P.
PR	21-NOV-2001;	2001US-0352468P.
PR	29-NOV-2001;	2001US-0354393P.
PR	03-DEC-2001;	2001US-0355394P.
PR	14-DEC-2001;	2001US-0340376P.
PR	08-JAN-2002;	2002US-0347211P.
PR	10-JAN-2002;	2002US-0347349P.
PR	08-FEB-2002;	2002US-0355250P.
PR	13-FEB-2002;	2002US-0356714P.
PR	20-FEB-2002;	2002US-0359077P.
PR	29-MAR-2002;	2002US-0356809P.
PR	04-APR-2002;	2002US-0370110P.
PR	12-APR-2002;	2002US-0372246P.
PR	05-JUN-2002;	2002US-0386614P.
PR	16-JUL-2002;	2002US-0396839P.
PR	22-JUL-2002;	2002US-0397775P.
PR	22-JUL-2002;	2002US-0397845P.
PR	09-SEP-2002;	2002US-0409450P.
XX	(EOSB-) EOS BIOTECHNOLOGY INC.	
PA		
XX		
PI	Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;	
PI	Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;	
XX		
DR	WPI; 2003-468649/44.	
XX		
DR	P-PSDB; ADN39997.	
XX		
PT	Determining the presence or absence of a pathological cell in a patient,	
PT	useful for diagnosing, prognosing or treating cancer, comprises detecting	
PT	a nucleic acid in a biological sample.	
XX		
PS	Claim 8; SEQ ID NO C152; 1385pp; English.	
XX		
CC	The invention relates to nucleic acids and proteins (ADN38683-ADN40064)	
CC	whose expression is upregulated or downregulated in specific cancers or	
CC	other diseases such as angiogenic or fibrotic disorders, and to methods	
CC	of determining the presence or absence of a pathological cell in a	
CC	patient by detecting a nucleic acid at least 80% identical to those of	
CC	the invention or by detecting a polypeptide of the invention. The	
CC	invention also relates to expression vectors and host cells comprising a	
CC	nucleic acid of the invention; antibodies which specifically bind a	
CC	polypeptide of the invention; use of such antibodies for drug targeting;	
CC	and methods of screening for modulators of activity or expression of the	
CC	polypeptides and nucleic acids. The nucleic acids, polypeptides,	
CC	antibodies and methods are useful for diagnosing, prognosing and treating	
CC	cancer and other conditions such as psoriasis, ischaemia, heart disease,	
CC	atherosclerosis, inflammatory diseases, autoimmune diseases, retinal	
CC	neovascularisation syndromes, scarring and uterine fibroids. They may	
CC	also be useful in wound healing and in contraception. The present	
CC	sequence represents a nucleic acid sequence of the invention.	
XX		
XX		
SEQ	Sequence 1451 BP; 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other;	
XX		
Query Match	90.0%; Score 1273; DB 11; Length 1451;	
Best Local Similarity	97.7%; Pred. No. 0;	
Matches 1291; Conservative	0; Mismatches 30; Indels 0; Gaps 0;	
29	GGCGAATTCGATCCAGGAGATGGGAGCCCGCGGCGTGGCTGCGGGGCGCC	88
127	GGCGTCGGGGCTTCCAGGAGGATGGAGCCCGCGGCGTGGCTGCGGGGCGCC	186
89	ATCTGTGACGAGCCTCTCTCTCTGTGACGTGGACCAATCCAAAGAACCAATAGATCTCT	148
187	ATCTGTGACGAGCCTCTCTCTCTGTGACGTGGACCAATCCAAAGAACCAATAGATCTCT	246
149	AAAGGAGAACCTTATTTGTTAGGTTGATGGACATCCACGTCACCTGAAAAAGAGTT	208
247	AAAGGAGAACCTTATTTGTTAGGTTGATGGACATCCACGTCACCTGAAAAAGAGTT	306
209	ACAGTTGAAAAAGCTTTTCTGTGTGATGAGTTTCTGTGATGTCCTCGCGTGGAAAACTG	268
307	ACAGTTGAAAAAGCTTTTCTGTGTGATGAGTTTCTGTGATGTCCTCGCGTGGAAAACTG	366

Qy	269	ACGACGTGCTTCCTTCCAAATGTGTCAACAATGGTGTGGGAGGAGTTGGCAAGTAAAC	328
Dp	367	ACGAGGCTCTTCCTCAATGTCTCAACAATGGTGTGGGAGGAGTTGGCAAGTAAAC	426
Qy	329	GGCATGGCCCTATGGGCTCTTCTTTCCGAATAGAGAAAGCAACCCTGCTGTGATTTAC	388
Dp	427	GGCATGGCCCTGTGGGCTCTTCTTTCCGAATAGAGAAAGCAACCCTGCTGTGATTTAC	486
Qy	389	ATGGCAATCTGGCCTTGGCTGACCTCTCTCTGTCACTGGTTCCCTTGAAGATTGCC	448
Dp	487	ATGGCAATCTGGCCTTGGCTGACCTCTCTCTGTCACTGGTTCCCTTGAAGATTGCC	546
Qy	449	TATCACAATACATGCGAACAATGTGATTAATGGGGAAGCTCTTGTAAATGTCTTATGGC	508
Dp	547	TATCACAATACATGCGAACAATGTGATTAATGGGGAAGCTCTTGTAAATGTCTTATGGC	606
Qy	509	TTTTTCTATCCCAACATGATGATCTGATTCCTTCACTGACCTGCTCAGTGTGAGAGG	568
Dp	607	TTTTTCTATGCGACATGATGATCTGATTCCTTCACTGACCTGCTCAGTGTGAGAGG	666
Qy	569	TATTGGGTCATCTGTGAACCCCATGGGGCACTTCAGAGAAAGGCAAACTTGGCAATTGGC	628
Dp	667	TATTGGGTCATCTGTGAACCCCATGGGGCACTTCAGAGAAAGGCAAACTTGGCAATTGGC	726
Qy	629	ATCTTCCTGGCAATATGGCTGTGACTCTGTGTGTCAACATCCCTTGTATGTGTGTAAG	688
Dp	727	ATCTTCCTGGCAATATGGCTGTGACTCTGTGTGTCAACATCCCTTGTATGTGTGTAAG	786
Qy	689	CAGACCAATCTTCATTCCTGGCCCTGGAACAACGACCTGTCAATGAATGTTTGTGCTGAGAG	748
Dp	787	CAGACCAATCTTCATTCCTGGCCCTGGAACAACGACCTGTCAATGAATGTTTGTGCTGAGAG	846
Qy	749	CTCTTGGTGGAGACATGTTCAATTACTTCTCTCTCTGAGCAATGGGGATCTTCTGTTC	808
Dp	847	CTCTTGGTGGAGACATGTTCAATTACTTCTCTCTCTGAGCAATGGGGATCTTCTGTTC	906
Qy	809	CCAGCCTTCTTCAACAGCCTTGTCTATGTGCTGATATCAGATGTGCGATCTTGTGCC	868
Dp	907	CCAGCCTTCTTCAACAGCCTTGTCTATGTGCTGATATCAGATGTGCGATCTTGTGCC	966
Qy	869	ATGATGAGAACTCGAGAGAGAAAGAAAGGGGCATCAACTATGTCACTGTCCCTG	928
Dp	967	ATGATGAGAACTCGAGAGAGAAAGAAAGGGGCATCAACTATGTCACTGTCCCTG	1026
Qy	929	GGCATGTACCTGATCTGCTTCACTCTCTGTAACTTCTGCTGTGAGTCAATATTTCTG	988
Dp	1027	GGCATGTACCTGATCTGCTTCACTCTCTGTAACTTCTGCTGTGAGTCAATATTTCTG	1086
Qy	989	ATTAAAGCCAGGGCCAGAGCAATGTCTATGCTATGACCTTATGACCTCTGCTCTCT	1048
Dp	1087	ATTAAAGCCAGGGCCAGAGCAATGTCTATGCTATGACCTTATGACCTCTGCTCTCT	1146
Qy	1049	ACCTTTAACAGCTGATGATGACCCCTTGTGTCTATTACTTGTGTTTCAATGATTTCAAGGAT	1108
Dp	1147	ACCTTTAACAGCTGATGATGACCCCTTGTGTCTATTACTTGTGTTTCAATGATTTCAAGGAT	1206
Qy	1109	CATGCAAAAGAACGCTCTCTTGGCCGAAGTGTCCGCACTGTAAAGCAATGCAAGTACCC	1168
Dp	1207	CATGCAAAAGAACGCTCTCTTGGCCGAAGTGTCCGCACTGTAAAGCAATGCAAGTACCC	1266
Qy	1169	CTCACTCTAAAGAAACATCTCCAGAAATTCAGACTCTTACTCTTCAAGTTCAACACTGTT	1228
Dp	1267	CTCACTCTAAAGAAACATCTCCAGAAATTCAGACTCTTACTCTTCAAGTTCAACACTGTT	1326
Qy	1229	AAAGACTCTCTATTTGAGTTTTCAGGTCCTCAGATGGGAATTGCAACGTAGAGATGTGAAAC	1288
Dp	1327	AAAGACTCTCTATTTGAGTTTTCAGGTCCTCAGATGGGAATTGCAACGTAGAGATGTGAAAC	1386
Qy	1289	CTGTTTAAATGATTAAGAGACGATCTGTATTTCCGGAATCCAGATCTTATTAAGACAA	1348
Dp	1387	CTGTTTAAATGATTAAGAGACGATCTGTATTTCCGGAATCCAGATCTTATTAAGACAA	1446

OY		1349 C 1349	
DB		1447 C 1447	
RESULT 8			
ID	ADRA46617	standard; DNA; 1451 BP.	
XX	ADRA46617,		
AC			
XX			
DT	18-NOV-2004	(first entry)	
XX			
DE	Cancer-associated protein coding sequence, SEQ ID 30.		
XX			
KW	Cytostatic; Gene Therapy; cancer; human; gene; ds.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	148..1341	
FT		/tag= A	
FT		/product= "Cancer-associated protein, SEQ ID 88"	
PX	WO2004073657-A2.		
PD	02-SEP-2004.		
XX			
PF	19-FEB-2004; 2004WO-US005455.		
XX			
PR	19-FEB-2003; 2003US-0448784P.		
XX			
PA	(PROT-) PROTEIN DESIGN LABS INC.		
PI	Aziz N, Gish KC, Wilson KE, Zlotnick A;		
XX			
DR	WPJ; 2004-652787/63.		
XX	P-PSDB; ADRA46675.		
PT	Detecting a pathological cell in a patient for diagnosing or treating		
PT	cancer by detecting in a biological sample from the patient genes whose		
PT	expression are up-regulated or down-regulated in specific cancers.		
XX			
PS	Claim 1; SEQ ID NO 30; 375bp; English.		
CC	The present invention relates to a method for detecting cancer in a		
CC	patient. The method comprises detecting in a biological sample from the		
CC	patient a nucleotide or protein sequence comprising a sequence that is at		
CC	least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or		
CC	protein sequence (ADR46646-ADR46703). The method is useful for detecting		
CC	cancer for preparing a composition for diagnosing or treating cancer.		
XX			
SEQ	Sequence 1451 BP; 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other;		
Query Match	90.0%; Score 1273; DB 13; Length 1451;		
Best Local Similarity	97.7%; Pred. No. 0;		
Matches 1291; Conservative	0; Mismatches 30; Indels 0; Gaps 0;		
OY	29 GGCGAATTGGATGCCAGAGGATGCGAGCCCCGCGCGGTGCTGCGGGGGCGGC	88	
DB	127 GGCGTCGGGGTTCCAGAGAGATCGGAGCCCCGCGCGGTGCTGCGGGGGCGGC	186	
OY	89 ATCTGCTAGACGCTCTCTCTCTGCAGTGGCACCATCCAAAGAACCAATAGATCTCT	148	
DB	187 ATCTGCTAGACGCTCTCTCTCTGCAGTGGCACCATCCAAAGAACCAATAGATCTCT	246	
OY	149 AAAGAAGAAAGCTTAATTGGTAGTGATGGACATCCCACTCACTGAAGAAAGATT	208	
DB	247 AAAAGAAGAAAGCTTAATTGGTAGTGATGGACATCCCACTCACTGAAGAAAGATT	306	
OY	209 ACAATTGAAAACGCTTTTCTGAGGAGAGATTTTTCGACTGTGCTCGTGAAGAACTG	268	
DB	307 ACAATTGAAAACGCTTTTCTGAGGAGAGATTTTTCGACTGTGCTCGTGAAGAACTG	366	

OY	269	ACACATGCTTCCTCCAAATGTGTCAACAATTTGGTGTGGGGGTTTTCGAAGTAC	328
Db	367	ACACAGGCTTCTTCCTCAATGTGTCAACAATTTGGTGTGGGGGTTTTCGAAGTAC	426
OY	329	GGCATAGCCCAATGGGTCTTTCCTTCCGAATAGAAAGACCCCTGCTGTATTTAC	388
Db	427	GGCATAGCCCTGTGGGTCTTTCCTTTCGGAATAGAAAGACCCCTGCTGTATTTAC	486
OY	389	ATGGCGAATCTGGCCTTGGCTGACCTCTCTGTGATCTGTGTTCCCTTGAAGTTGCC	448
Db	487	ATGGCGAATCTGGCCTTGGCTGACCTCTCTGTGATCTGTGTTCCCTTGAAGTTGCC	546
OY	449	TATCACATACATGGCAACAATGATTTATGGGGAAGCTCTTGTAAATGTCTTATTTGGC	508
Db	547	TATCACATACATGGCAACAATGATTTATGGGGAAGCTCTTGTAAATGTCTTATTTGGC	606
OY	509	TTTTTCTATCGCAATGTAATCTGTTCCATTTCTCTTATGACCTGCTCAGTGTGCAAGG	568
Db	607	TTTTTCTATGCGAATGTAATCTGTTCCATTTCTCTTATGACCTGCTCAGTGTGCAAGG	666
OY	569	TATTGGGATCATCGTGAACCCCATGGGGGACATCCAGAAAGAGGCAAACTTGGCATTTGGC	628
Db	667	TATTGGGATCATCGTGAACCCCATGGGGGACATCCAGAAAGAGGCAAACTTGGCATTTGGC	726
OY	629	ATCTCCCTGGCAATATGGCTGTGAATCTGTGTGTGACATCTCTTGTATGTGTGAAG	688
Db	727	ATCTCCCTGGCAATATGGCTGTGAATCTGTGTGTGACATCTCTTGTATGTGTGAAG	786
OY	689	CAGACCATCTTCATCTCCCTGGCCCTGAACATCAAGACCTGTCAATGATTTTGGCTGAAGG	748
Db	787	CAGACCATCTTCATCTCCCTGGCCCTGAACATCAAGACCTGTCAATGATTTTGGCTGAAGG	846
OY	749	CTCTTGTGTGGAGACATGTTCAATTACTTCTCTCTCTGAGCAATTTGGGGTCTTTCGTTC	808
Db	847	CTCTTGTGTGGAGACATGTTCAATTACTTCTCTCTCTGAGCAATTTGGGGTCTTTCGTTC	906
OY	809	CCAGGCTTCTTCACAGGCTCTGGCTTAATGTGCTGATGATCAGAAATGCTGGCATTTCTGCC	868
Db	907	CCAGGCTTCTTCACAGGCTCTGGCTTAATGTGCTGATGATCAGAAATGCTGGCATTTCTGCC	966
OY	869	ATGATATGAAATCTCAGAGAAGAAAGAAAGAGGGGCATCAAACTATGTCACTGTCTGT	928
Db	967	ATGATATGAAATCTCAGAGAAGAAAGAAAGAGGGGCATCAAACTATGTCACTGTCTGT	1026
OY	929	GGCATATGACTGATCTGCTTCACTCTCTAGTAACTTCTGTGTGTGTGATTAATTTCTG	988
Db	1027	GGCATATGACTGATCTGCTTCACTCTCTAGTAACTTCTGTGTGTGTGATTAATTTCTG	1086
OY	989	ATTAGAGCCGAGGGCAGAGCCATGTCTAATGCCCTGTACATTTGAGCCCTGTCTCT	1048
Db	1087	ATTAGAGCCGAGGGCAGAGCCATGTCTAATGCCCTGTACATTTGAGCCCTGTCTCT	1146
OY	1049	ACCCTTAAACAGCTGATCGACCCCTTGTGTCTAATTACTTGTGTTGACATGATTTGAGGAT	1108
Db	1147	ACCCTTAAACAGCTGATCGACCCCTTGTGTCTAATTACTTGTGTTGACATGATTTGAGGAT	1206
OY	1109	CATGCAAAAGAACGCTCTCTCTTGTCCGAAGTGTCCGACATGTAAAGCAGATGCAGTACCC	1168
Db	1207	CATGCAAAAGAACGCTCTCTCTTGTCCGAAGTGTCCGACATGTAAAGCAGATGCAGTACCC	1266
OY	1169	CTCAACCTCAAAAGAAACATCCAGAGAAATCCAGGCTTACTTCACTTCAAGTTCAACACAGTGT	1228
Db	1267	CTCAACCTCAAAAGAAACATCCAGAGAAATCCAGGCTTACTTCACTTCAAGTTCAACACAGTGT	1326
OY	1229	AAAGACTCTTATGAGTTTTCAGAGTCTCTCAGATGGGAATTTGACAGTAGATGTGAAC	1288
Db	1327	AAAGACTCTCTATGAGTTTTCAGAGTCTCTCAGATGGGAATTTGACAGTAGATGTGAAC	1386
OY	1289	CTGTTTAATGTTATAGAGACGGTCTGTGTTATTTCCGATTCAGATCTTATTAAGCGAGAA	1348
Db	1387	CTGTTTAATGTTATAGAGACGGTCTGTGTTATTTCCGATTCAGATCTTATTAAGCGAGAA	1446

QY	1349	C 1349	
Db	1447	C 1447	
RESULT 9			
ADST74019			
ID	ADST74019	standard; cDNA; 1451 BP.	
XX			
AC	ADST74019;		
XX			
DT	16-DEC-2004	(first entry)	
XX			
DE	Human G-protein coupled proteinase activated receptor 2 polynucleotide.		
XX			
KW	Human; proteinase activated receptor 2; PAR2; G-protein coupled receptor;		
KW	receptor; cardiac; neuroprotective; nephrotropic; respiratory-gen. ;		
KW	gastrointestinal-gen.; gene therapy; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	148..1341	
FT		/tag= a	
FT		/product= "Human PAR2"	
PN	WO2004080373-A2.		
XX			
PD	23-SEP-2004.		
XX			
PF	26-FEB-2004; 2004WO-EP001896.		
XX			
PR	11-MAR-2003; 2003EP-00004980.		
XX			
PA	(FARB) BAYER HEALTHCARE AG.		
XX			
PI	Golz S, Brueggemeier U, Summer H;		
XX			
DR	WPI; 2004-677358/66.		
XX	P-PsDB; ADST74020.		
PT	Screening for therapeutic agents for treating e.g., cardiovascular		
PT	diseases by contacting a test compound with a proteinase activated		
PT	receptor 2 (PAR2) polypeptide or polynucleotide and detecting binding of		
PT	the test compound.		
PS	Disclosure; SEQ ID NO 1, 121pp; English.		
XX			
CC	The present sequence is that of a polynucleotide encoding G-protein		
CC	coupled proteinase activated receptor 2 (PAR2). PAR2 is an		
CC	antiinflammatory receptor in the colon and may also play a role in the		
CC	airway, regulating sodium ion absorption and anion secretion. The		
CC	invention relates to novel disease associations of PAR2 polypeptides and		
CC	polynucleotides. It also relates to novel methods of screening for		
CC	therapeutic agents for the treatment of cardiovascular disorders,		
CC	gastrointestinal and liver diseases, neurological disorders, urological		
CC	disorders, hematological diseases and respiratory diseases in a mammal.		
CC	Suitable therapeutic agents include a small molecule, an RNA molecule, an		
CC	antisense oligonucleotide, a polypeptide, an antibody or a ribozyme. The		
CC	invention also provides pharmaceutical compositions for the treatment of		
CC	diseases and disorders associated with PAR2 comprising a PAR2		
CC	polypeptide, PAR2 polynucleotide or a regulator or modulator of PAR2		
CC	activity. Methods of diagnosing these diseases and disorders involve		
CC	determining the amount of PAR2 polynucleotide in a sample.		
XX			
SEQ	Sequence 1451 BP, 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other;		
Query Match	90.0%; Score 1273; DB 13; Length 1451;		
Best Local Similarity	97.7%; Pred. No. 0;		
Matches 1291;	Conservative 0; Mismatches 30; Indels 0; Gaps 0;		
29	GCGGATTGCGATCCAGAGGATGCGAGCCCGGCGCGGCTGCTCTGCGGCGCC		

CC treatment methods, and prognosis. The gene or protein expression profile
CC may also be used for creating microarrays. The microarray is useful for
CC genetic and physical mapping of genomes, DNA sequencing, genetic or
CC medical diagnosis, genotyping of organisms, confirming cell or tissue
CC identifications and in identifying promising antibiotics, antiviral or
CC antifungal agents

XX Sequence 2848 BP; 670 A; 562 C; 552 G; 771 T; 0 U; 293 Other;

Query Match 89.4%; Score 1263.6; DB 6; Length 2848;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 29 GCGGAATTCGATTCAGAGAGATGCGAGCCCGAGCGCGGCTGCTGGGGGCGCC 88
DB 126 GCGGTGGGGCTTCCAGAGAGATGCGAGCCCGAGCGCGGCTGCTGGGGGCGCC 185
QY 89 ATCTCTCTAGCAGCCTCTCTCTCTGCAATGCGACCAATCCAGAACCAATATCTCT 148
DB 186 ATCTCTCTAGCAGCCTCTCTCTCTGCAATGCGACCAATCCAGAACCAATATCTCT 245
QY 149 AAGAGAGAGCCTTATGTTAGTTGATGAGCAATCCAGCTCACT-GGAAAGAGT 207
DB 246 AAGAGAGAGCCTTATGTTAGTTGATGAGCAATCCAGCTCACTGGGAAAGAGT 305
QY 208 TACAGTTGAAACAGTCTTTCTGATGATGATGATGATGATGATGATGATGATGAT 267
DB 306 TACAGTTGAAACAGTCTTTCTGATGATGATGATGATGATGATGATGATGATGAT 365
QY 268 GACCACTGCT 327
DB 366 GACCACTGCT 425
QY 328 CGCATGCGCCCTATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 387
DB 426 CGCATGCGCCCTATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 485
QY 388 CATGGCAATCTGGCCTTGGCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 447
DB 486 CATGGCAATCTGGCCTTGGCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 545
QY 448 CTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 507
DB 546 CTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 605
QY 508 CTTTTCATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
DB 606 CTTTTCATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 665
QY 568 GTATTGGGTCTATGTAACCCCATGGGGCATCTCAGAGAGAGAGAGAGAGAGAGAG 627
DB 666 GTATTGGGTCTATGTAACCCCATGGGGCATCTCAGAGAGAGAGAGAGAGAGAGAG 725
QY 628 CATCTCCCTGGCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 687
DB 726 CATCTCCCTGGCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 785
QY 688 GCAGACCATCTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 747
DB 786 GCAGACCATCTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 845
QY 748 GCTCTTGGTGGAGACATGTTCAATTAATCTCTCTCTGCGCATGAGGCTCTTCTGTT 807
DB 846 GCTCTTGGTGGAGACATGTTCAATTAATCTCTCTCTGCGCATGAGGCTCTTCTGTT 905
QY 808 CCGAGCCTTCTCAAGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867
DB 906 CCGAGCCTTCTCAAGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 965
QY 868 CATGATGAGAACTCAG 927
DB 966 CATGATGAGAACTCAG 1025

QY 928 GCGCATGATCATGATCTGCTTCACTCTCTATGTAACCTTCTGCTTGGTGCATATTCTTCT 987
DB 1026 GCGCATGATCATGATCTGCTTCACTCTCTATGTAACCTTCTGCTTGGTGCATATTCTTCT 1085
QY 988 GATTAAAGCCAGGGCCAGAGCATGTCATGCCCCGTGATCATGTAAGCCCTGACCTCTC 1047
DB 1086 GATTAAAGCCAGGGCCAGAGCATGTCATGCCCCGTGATCATGTAAGCCCTTGCCTCTC 1145
QY 1048 TACCTTTAACAGCTGATGAGACCCCTTGTCTATTAATCTTGTGTTCAATGATTTGAGGA 1107
DB 1146 TACCTTTAACAGCTGATGAGACCCCTTGTCTATTAATCTTGTGTTCAATGATTTGAGGA 1205
QY 1108 TCATGGAAGAACGCTCTCTCTTTCGCCAAGTGTCCGCACTGTAAGCAATGCAATGAC 1167
DB 1206 TCATGGAAGAACGCTCTCTCTTTCGCCAAGTGTCCGCACTGTAAGCAATGCAATGAC 1265
QY 1168 CCTCACTCAAGAAACAATCCAGAGAAATCCAGCTCTTACTCTTCAAGTTCAACCACTGT 1227
DB 1266 CCTCACTCAAGAAACAATCCAGAGAAATCCAGCTCTTACTCTTCAAGTTCAACCACTGT 1325
QY 1228 TAAGACCTCTATGATGATTTTCCAGGTCTCTCAGATGGGAATTGCAAGTGAATGTGAA 1287
DB 1326 TAAGACCTCTATGATGATTTTCCAGGTCTCTCAGATGGGAATTGCAAGTGAATGTGAA 1385
QY 1288 CCTGTTTAATGTTAAGAGAGAGTGTCTGTTATTTCCGATCCAGATCTTATTAAAGACA 1347
DB 1386 CCTGTTTAATGTTAAGAGAGAGTGTCTGTTATTTCCGATCAAAAGGTCTCACCAATTA 1445
QY 1348 ACTGTTTAT 1357
DB 1446 CATGTGAT 1455

RESULT 11
AAD4437
ID AAD4437 standard; DNA; 8624 BP.
XX
AC AAD4437;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human coagulation factor II (thrombin) receptor like 1 (F2RL1) gene.
XX
KW Human; haplotype; coagulation factor II receptor like 1; F2RL1; asthma;
KW polymorphism; chronic pulmonary disease; inflammatory disorder;
KW gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key
FT Location/Qualifiers
FT replace(517, G)
FT /tag= a
FT /note= "Polymorphic site; PS1"
FT replace(553, C)
FT /tag= b
FT /note= "Polymorphic site; PS2"
FT replace(768, T)
FT /tag= c
FT /note= "Polymorphic site; PS3"
FT replace(850, T)
FT /tag= d
FT /note= "Polymorphic site; PS4"
FT replace(852, G)
FT /tag= e
FT /note= "Polymorphic site; PS5"
FT 1001..7382
FT /tag= f
FT CDS
FT /tag= f
FT /product= "Human F2RL1 protein"
FT 1001..1082
FT /tag= g
FT /number= 1
FT 1083..6270
FT /tag= h
FT Intron

FT exon 6271..7382
 FT /*tag= 1
 FT /number= 2
 FT variation replace(6277, G)
 FT /*tag= 1
 FT /note= "Polymorphic site; PS6"
 FT replace(6809, T)
 FT /*tag= k
 FT /note= "Polymorphic site; PS7"
 FT replace(7460, C)
 FT /*tag= 1
 FT /note= "Polymorphic site; PS8"
 PN MO200255534-A2.
 PD 18-JUL-2002.
 XX 13-NOV-2001, 2001MO-US046475.
 PF 10-NOV-2000, 2000US-0247516P.
 XX (GENA-) GENA155ANCB PHARM INC.
 PA Blegiecki KM, Sanchez A, Shah N;
 PI WPI, 2002-566728/60.
 XX P-PSDB; AA026678.
 DR
 XX New genetic variants having polymorphisms in the coagulation factor II
 PT (chrombin) receptor like 1 (F2RL1) gene, useful for studying the function
 PT of F2RL1 and treating disorders associated with abnormal expression or
 PT function of F2RL1.
 XX
 PS Claim 18; Fig 1; 65p; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising genes and
 CC haplotypes of the coagulation factor II (thrombin) receptor like 1
 CC (F2RL1) gene. Polymorphic variants of the F2RL1 gene are useful in
 CC studying the expression and biological function of F2RL1, and in
 CC identifying the expression and biological function of F2RL1, e.g. asthma,
 CC associated with abnormal expression or function of F2RL1, e.g. asthma,
 CC chronic pulmonary disease, and inflammatory disorders. Polynucleotides
 CC comprising a polymorphic gene variant or fragment may be used for
 CC therapeutic purposes, where a patient could benefit from expression or
 CC increased expression of a particular F2RL1 protein isoform, or an
 CC expression vector encoding the isoform may be administered to the
 CC patient. Haplotype information is useful in improving the efficiency and
 CC output of several steps in drug discovery and development process,
 CC including target validation, identifying lead compounds, and early phase
 CC clinical trials. Information on polymorphisms may be applied in studying
 CC biological functions of F2RL1 as well as in identifying drugs targeting
 CC this protein for the treatment of disorders related to its abnormal
 CC expression or function. The invention is useful in gene therapy. The
 CC present sequence is human F2RL1 gene
 XX
 SO Sequence 8624 BP; 2126 A; 2010 C; 1988 G; 2392 T; 0 U; 108 Other;
 Query Match 84.0%; Score 1188.4; DB 6; Length 8624;
 Best Local Similarity 97.8%; Pred. No. 0;
 Matches 1201; Conservative 3; Mismatches 24; Indels 0; Gaps 0;
 QY 130 AGGACCAATGATCTCTTAAGAGAGAGCCCTTATGTTGATGATGACATATCCCA 189
 DB AGGACCAATGATCTCTTAAGAGAGAGCCCTTATGTTGATGATGACATATCCCA 6328
 QY 190 CGTCACTGAAAAAGAGTTACAGTTGAACAGTCTTTCTGTGATGAGTTTCTGCATC 249
 DB CGTCACTGAAAAAGAGTTACAGTTGAACAGTCTTTCTGTGATGAGTTTCTGCATC 6388
 QY 250 TGTCTCTGCTGAAAACTGACCACTGCTCTTCCATTGCTACCAATGCTGTTGC 309
 DB TGTCTCTGCTGAAAACTGACCACTGCTCTTCCATTGCTACCAATGCTGTTGT 6448

QY 310 GGTGGGTTTCCAGTAAAGGAGAGCCCTATGGATCTTCTCTTTCGAACTAAGAGAA 369
 DB GGTGGGTTTCCAGTAAAGGAGAGCCCTATGGATCTTCTCTTTCGAACTAAGAGAA 6508
 QY 370 GCAACCTGCTGATTTTACATGACCAATCTGACCTTGTGACCTCTCTGATCTG 429
 DB GCAACCTGCTGATTTTACATGACCAATCTGACCTTGTGACCTCTCTGATCTG 6568
 QY 430 GTTCCCTGAAATGACCTATACATATGACCAATGACCAATGACCTATGATTTT 489
 DB GTTCCCTGAAATGACCTATACATATGACCAATGACCAATGACCTATGATTTT 6628
 QY 490 TTGTAATGCTATTTGCTTTTCTTATGCAATGATCTGTTCTTCTTCTTAC 549
 DB TTGTAATGCTATTTGCTTTTCTTATGCAATGATCTGTTCTTCTTCTTAC 6688
 QY 550 CTGCTCACTGTCAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 609
 DB CTGCTCACTGTCAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 6748
 QY 610 GGCACATTTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 669
 DB GGCACATTTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 6808
 QY 6749 GGCACATTTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 6808
 DB GGCACATTTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 6868
 QY 670 CCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
 DB CCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6868
 QY 730 TGAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 789
 DB TGAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6928
 QY 790 TGAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 849
 DB TGAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6928
 QY 850 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 909
 DB AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7048
 QY 910 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 969
 DB ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7108
 QY 970 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1029
 DB TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7168
 QY 1030 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1089
 DB TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7228
 QY 1090 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1149
 DB TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7288
 QY 1150 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1209
 DB AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7348
 QY 1210 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1269
 DB TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7408
 QY 1270 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1329
 DB GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7468
 QY 1330 AGATCTTATTAAGCAAGACTTGTAT 1357
 DB AGATCTTATTAAGCAAGACTTGTAT 7496

RESULT 12
 AAD4438
 ID AAD4438 standard; DNA; 1194 BP.
 XX
 AC AAD4438;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human coagulation factor II (thrombin) receptor like 1 (F2RL1) DNA.
 XX
 KM Human: haplotype; coagulation factor II receptor like 1; F2RL1; asthma;
 KW polymorphism; chronic pulmonary disease; inflammatory disorder;
 KM gene therapy; gene; db.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1194
 FT /tag= a
 FT /product= "Human F2RL1 protein"
 FT /replace(89, G)
 FT /tag= b
 FT /note= "Polymorphic site"
 FT /replace(621, T)
 FT /tag= c
 FT /note= "Polymorphic site"
 PN MO20025534-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 13-NOV-2001; 2001MO-US046475.
 XX
 PR 10-NOV-2000; 2000US-0247516P.
 XX
 PA (GENA-) GENA/ISSANCE PHARM INC.
 XX
 PI Bieglecki KM, Sanchis A, Shah N;
 XX
 DR WPI; 2002-566728/60.
 DR P-PSDB; AAE26678.
 XX
 PT New genetic variants having polymorphisms in the coagulation factor II
 PT (thrombin) receptor like 1 (F2RL1) gene, useful for studying the function
 PT of F2RL1 and treating disorders associated with abnormal expression or
 PT function of F2RL1.
 XX
 PS Claim 23; Fig 2; 65pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising genes and
 CC haplotypes of the coagulation factor II (thrombin) receptor like 1
 CC (F2RL1) gene. Polymorphic variants of the F2RL1 gene are useful in
 CC studying the expression and biological function of F2RL1, and in
 CC identifying drugs targeting F2RL1 protein for treating disorders
 CC associated with abnormal expression or function of F2RL1, e.g. asthma,
 CC chronic pulmonary disease, and inflammatory disorders. Polynucleotides
 CC comprising a polymorphic gene variant or fragment may be used for
 CC therapeutic purposes, where a patient could benefit from expression or
 CC increased expression of a particular F2RL1 protein isoform, or an
 CC expression vector encoding the isoform may be administered to the
 CC patient. Haplotype information is useful in improving the efficiency and
 CC output of several steps in drug discovery and development process,
 CC including target validation, identifying lead compounds, and early phase
 CC clinical trials. Information on polymorphisms may be applied in studying
 CC biological functions of F2RL1 as well as in identifying drugs targeting
 CC this protein for the treatment of disorders related to its abnormal
 CC expression or function. The invention is useful in gene therapy. The
 CC present sequence is human F2RL1 DNA
 XX
 SO Sequence 1194 BP; 264 A; 321 C; 261 G; 348 T; 0 U; 0 Other;

Matches 1187; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 50 ATGCGAGCCCGCAGCGCGCTGCTGCTGCGGCGCCCATCTGCTAGACGCTCTCTC 109
 DB 1 ATGCGAGCCCGCAGCGCGCTGCTGCTGCGGCGCCCATCTGCTAGACGCTCTCTC 60
 QY 110 TCCTGCACTGCGCACATCCAGAACCAATAGATCTCTTAAGGAAGAACCTTATTGGT 169
 DB 61 TCCTGCACTGCGCACATCCAGAACCAATAGATCTCTTAAGGAAGAACCTTATTGGT 120
 QY 170 AAGGTGATGAGCACATCCACGCTCACTGGAAGAGAGTTACAGTTAAACAGTCTTCTC 229
 DB 121 AAGGTGATGAGCACATCCACGCTCACTGGAAGAGAGTTACAGTTAAACAGTCTTCTC 180
 QY 230 GTGATGAGTTTCTGCACTGCTGCTGCTGCAAACTGACCACTGCTCTCTTCCAAAT 289
 DB 181 GTGATGAGTTTCTGCACTGCTGCTGCTGCAAACTGACCACTGCTCTCTTCCAAAT 240
 QY 290 GTCTACCAATGTGTTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 349
 DB 241 GTCTACCAATGTGTTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 300
 QY 350 CTTTTCGAACTTAAGAAAGAACCCCTGCTGATTTTACATGGCCCAATGCGCTGGCT 409
 DB 301 CTTTTCGAACTTAAGAAAGAACCCCTGCTGATTTTACATGGCCCAATGCGCTGGCT 360
 QY 410 GACCTCTCTCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 469
 DB 361 GACCTCTCTCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 470 TGGATTTAAGGGAAGCTCTTGTGTAATGTGCTTATTGCTTTTCTATGCAATGTATC 529
 DB 421 TGGATTTAAGGGAAGCTCTTGTGTAATGTGCTTATTGCTTTTCTATGCAATGTATC 480
 QY 530 TGTTCATCTCTCTCATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 589
 DB 481 TGTTCATCTCTCTCATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 590 ATGGGCACTCCAGAAAGGCAAACTTGGCATTTGGCATCTCCCTGGCAATATGCTG 649
 DB 541 ATGGGCACTCCAGAAAGGCAAACTTGGCATTTGGCATCTCCCTGGCAATATGCTG 600
 QY 650 CTGACTCTGCTGCTCAATCCCTTGTATGTGCTGTAAGACATCTTCACTCTGCTGCC 709
 DB 601 CTGACTCTGCTGCTCAATCCCTTGTATGTGCTGTAAGACATCTTCACTCTGCTGCC 660
 QY 710 CTGAACATACGACCTGTGATGATGTTTGGCTGAGACGCTCTGATGGGAGACATGTT 769
 DB 661 CTGAACATACGACCTGTGATGATGTTTGGCTGAGACGCTCTGATGGGAGACATGTT 720
 QY 770 AATTACTCTCTCTCTGCGCAATGGGGTCTTCTGTTCCAGCTTCTCTCAAGCTCT 829
 DB 721 AATTACTCTCTCTCTGCGCAATGGGGTCTTCTGTTCCAGCTTCTCTCAAGCTCT 780
 QY 830 GCTTATGTGCTGATGATCAAGATGTGCGATCTTCTGCAATGATGATAAATCTAGGAAG 889
 DB 781 GCTTATGTGCTGATGATCAAGATGTGCGATCTTCTGCAATGATGATAAATCTAGGAAG 840
 QY 890 AAAAGGAAGAGGCGCATCAACATCTGATGATGCTGCTGCTGCTGCTGCTGCTGCT 949
 DB 841 AAAAGGAAGAGGCGCATCAACATCTGATGATGCTGCTGCTGCTGCTGCTGCTGCT 900
 QY 950 ACTCTAGTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
 DB 901 ACTCTAGTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 1010 CATGCTATGACCTGTGATCAATGTAGCCCTGCTGCTCTCAACCTTAAACGCTGATCGAC 1069
 DB 961 CATGCTATGACCTGTGATCAATGTAGCCCTGCTGCTCTCAACCTTAAACGCTGATCGAC 1020
 QY 1070 CCTTTGCTATTAATCTTTGCTTCAATGATTTTCAAGGATGATGCAAGAAAGCTCTCTT 1129
 DB 1021 CCTTTGCTATTAATCTTTGCTTCAATGATTTTCAAGGATGATGCAAGAAAGCTCTCTT 1080

Query Match 83.6%; Score 1182.8; DB 6; Length 1194;
 Best Local Similarity 99.4%; Pred. No. 0;

QY 1130 TGCAGAGTCCGCACTGTAAAGCAGATGCAATCCCTACCTCAAGAAACACTCC 1189
DB 1081 TGCAGAGTCCGCACTGTAAAGCAGATGCAATCCCTACCTCAAGAAACACTCC 1140
QY 1190 AGGAATCCAGCTCTTAAGTTCAAGTTCAACCACTGTAAAGCTCTTAATGA 1243
DB 1141 AGGAATCCAGCTCTTAAGTTCAAGTTCAACCACTGTAAAGCTCTTAATGA 1194

RESULT 13
AAZ50773
ID AAZ50773 standard; DNA; 1289 BP.
XX AAZ50773;
AC
XX
XX 31-MAY-2000 (first entry)
XX
XX
XX Human protease activated receptor-2 DNA.
XX
XX Human, PAR-2; protease activated receptor; antisense molecule;
XX PAR antibody; cytostatic; therapeutic; metastatic tumour cell;
XX placental implantation; invasive cell; ds.
XX
XX Homo sapiens.
XX
XX MO200008150-A1.
XX
XX 17-FEB-2000.
XX
XX 05-FEB-1999; 99MO-IL000079.
XX
XX 07-AUG-1998; 98IL-00125698.
XX
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
XX Bar-Shavit R;
XX
XX WPI; 2000-205706/18.
XX
XX
XX Treating metastatic tumor cells useful for treating disorders involving
XX placenta implantation in a female comprises administration of an
XX antisense molecule complementary to an RNA sequence of a protease
XX activated receptor protein.
XX
XX Example 3; Fig 9; 46p; English.
XX
XX The patent discloses a method to treat metastatic tumour cells using an
XX antisense molecule comprising a polynucleotide complementary to an RNA
XX sequence of a protease activated receptor (PAR) protein, or an antibody
XX capable of binding to a PAR protein. The antisense molecules and
XX antibodies of PAR protein are also used to treat disorders associated
XX with implantation of placenta. The present sequence is a human PAR-2 DNA
XX used for producing antisense molecules for treating invasive cells

SO Sequence 1289 BP; 300 A; 320 C; 270 G; 399 T; 0 U; 0 Other;
Query Match 83.4%; Score 1182.8; DB 3; Length 1289;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1187; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 130 AGGAATCCAGCTCTTAAGTTCAAGTTCAACCACTGTAAAGCTCTTAATGA 189
DB 95 AGGAATCCAGCTCTTAAGTTCAAGTTCAACCACTGTAAAGCTCTTAATGA 154
QY 190 CGTCACTGAAAAGAGTTACAGTTGAAACAGTCTTTCTGTGATGAGTTTCTGCATC 249
DB 155 CGTCACTGAAAAGAGTTACAGTTGAAACAGTCTTTCTGTGATGAGTTTCTGCATC 214
QY 250 TGTCTCTGCTGAAAAGAGTTACAGTTGAAACAGTCTTTCTGTGATGAGTTTCTGCATC 309
DB 215 TGTCTCTGCTGAAAAGAGTTACAGTTGAAACAGTCTTTCTGTGATGAGTTTCTGCATC 274

QY 310 GGTGGGTTTCCAGATACCGGATGAGCCCTATGAGTCTTCTTCCGAATAGAGAA 369
DB 275 GGTGGGTTTCCAGATACCGGATGAGCCCTATGAGTCTTCTTCCGAATAGAGAA 334
QY 370 GCAACCTGCTGTGATTTACATGAGCAATCTGACCTTGTGACCTCTCTGTGATCTG 429
DB 335 GCAACCTGCTGTGATTTACATGAGCAATCTGACCTTGTGACCTCTCTGTGATCTG 394
QY 430 GTTCCCTGAAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAAT 489
DB 395 GTTCCCTGAAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAAT 454
QY 490 TTGTAATGATCTTATGAGCTTTTCTTATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAAT 549
DB 455 TTGTAATGATCTTATGAGCTTTTCTTATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAAT 514
QY 550 CTGCTCAAGTGTGAGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 609
DB 515 CTGCTCAAGTGTGAGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 574
QY 610 GGAAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAAT 669
DB 575 GGAAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAAT 634
QY 670 CCTTTGATGATGAGTGAAGAGCAATCTTCAATCTGACCTGAGCAATCAAGACTGTCA 729
DB 635 CCTTTGATGATGAGTGAAGAGCAATCTTCAATCTGACCTGAGCAATCAAGACTGTCA 694
QY 730 TGAATGTTTGCCTGAGAGAGCTTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 789
DB 695 TGAATGTTTGCCTGAGAGAGCTTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 754
QY 790 CATTTGGGCTTTCTGTTCCAGAGCTTCTCAAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 849
DB 755 CATTTGGGCTTTCTGTTCCAGAGCTTCTCAAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 814
QY 850 AATGCTGAGATCTTCTGAGCAATGAGTGAAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 909
DB 815 AATGCTGAGATCTTCTGAGCAATGAGTGAAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 874
QY 910 ACTCATTTGATCTGCTGAGGAGATGAGCTGATCTGCTTCACTCTAGTAACCTTGTGCT 969
DB 875 ACTCATTTGATCTGCTGAGGAGATGAGCTGATCTGCTTCACTCTAGTAACCTTGTGCT 934
QY 970 TGTGATGATTTATTTCTGATTTAAGAGCCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1029
DB 935 TGTGATGATTTATTTCTGATTTAAGAGCCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 994
QY 1030 TGTAGCCCTGCTGCTGATACCTTAAAGAGCTGATGAGAGCCCTTGTGATTAATCTTGT 1089
DB 995 TGTAGCCCTGCTGCTGATACCTTAAAGAGCTGATGAGAGCCCTTGTGATTAATCTTGT 1054
QY 1090 TTGACATGATTTGAGGAGATGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1149
DB 1055 TTGACATGATTTGAGGAGATGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1114
QY 1150 AAGGAGATGAGAGATACCTGATCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1209
DB 1115 AAGGAGATGAGAGATACCTGATCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1174
QY 1210 TTCAAGTTCAACAGCTTTAAGAGCTCTTATGAGTTTCAAGTCTGAGTCTGAGTGGAAAT 1269
DB 1175 TTCAAGTTCAACAGCTTTAAGAGCTCTTATGAGTTTCAAGTCTGAGTCTGAGTGGAAAT 1234
QY 1270 GCAAGATGAGATGAGAGAGCTGTTTATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1323
DB 1235 GCAAGATGAGATGAGAGAGCTGTTTATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1288

RESULT 14
ADO29874
ID ADO29874 standard; cDNA; 1194 BP.
XX

AC ADO29874;
 XX
 XX 29-JUL-2004 (first entry)
 XX
 XX Human GPCR F2RL1 polynucleotide, SEQ ID NO:976.
 DE
 XX
 XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
 KW cytotoxic; antiinflammatory; vasotropic; antiangiinal; antidiabetic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 KW dermatological; antidiuretic; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW gene; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2004040000-A2.
 PN
 XX
 XX 13-MAY-2004.
 PD
 XX
 XX
 XX 09-SEP-2003; 2003WO-US028226.
 PF
 XX
 XX 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX
 XX (PRIM-) PRIMAL INC.
 PA
 XX
 XX Galenatis GA, Bergmann JB, Gragerov A, Hohmann J, Li F,
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 XX
 XX MPI; 2004-390329/36.
 DR P-PSDB; ADO29311.
 XX
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 PT
 XX
 XX Claim 151; SEQ ID NO 976; 542pp; English.
 PS
 XX
 XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,

CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR encoding
 CC nucleic acid of the invention. Note: The full sequence data for this
 CC patent did not form part of the printed specification; those sequences
 CC not shown were obtained in electronic format directly from WIP0 at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 XX Sequence 1194 BP; 264 A; 322 C; 261 G; 347 T; 0 U; 0 Other;
 SQ
 Query Match 83.4%; Score 1179.6; DB 12; Length 1194;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1185; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 50 ATGCGAGGCCCAAGCGCGGCTGCTGCGGAGCGCCATCTGCTAGCAGCTCTCTC
 DB 1 ATGCGAGGCCCAAGCGCGGCTGCTGCGGAGCGCCATCTGCTAGCAGCTCTCTC 60
 QY 110 TCTGCAAGTGGCACTCCAGAAACCAATATCTCTAAAGAAAGAGCTTATGGCT 169
 DB 61 TCTGCAAGTGGCACTCCAGAAACCAATATCTCTAAAGAAAGAGCTTATGGCT 120
 QY 170 AAGTTGATGGACATCCCACTGCACTGGAAAAAGAGTTACAGTTGAACAGTCTTTCT 229
 DB 121 AAGTTGATGGACATCCCACTGCACTGGAAAAAGAGTTACAGTTGAACAGTCTTTCT 180
 QY 230 GTGATGAGTTTCTGCACTGTCTCTCGTGGAAAACTGACCACTGTCTTCTTCAAT 289
 DB 181 GTGATGAGTTTCTGCACTGTCTCTCACTGGAAAACTGACCACTGTCTTCTTCAAT 240
 QY 290 GTCTACAAATGTGTTCGGGTGGTTTGGCAAGTAAAGGCAATGGCCCTAAGGGCTTT 349
 DB 241 GTCTACAAATGTGTTCGGGTGGTTTGGCAAGTAAAGGCAATGGCCCTAAGGGCTTT 300
 QY 350 CTTTCCGAACCTAAGAAAGAACCCCTGCTGATTTACATGAGCCATCTGACCTTGACT 409
 DB 301 CTTTCCGAACCTAAGAAAGAACCCCTGCTGATTTACATGAGCCATCTGACCTTGACT 360
 QY 410 GACCTCTCTCTGTCATCTGTTTCCCTTGAAGATTGCTTATCAATATGAGCAAC 469
 DB 361 GACCTCTCTCTGTCATCTGTTTCCCTTGAAGATTGCTTATCAATATGAGCAAC 420
 QY 470 TGGATTATGGGGAAGCTTTTGTAAATGCTTATTTGGCTTTTTCATGCAACATGTC 529
 DB 421 TGGATTATGGGGAAGCTTTTGTAAATGCTTATTTGGCTTTTTCATGCAACATGTC 480
 QY 530 TGTTCATCTCTTCATGACCTGCTCACTGCTGAGAGGATATGGCTCATCTGTAACCC 589
 DB 481 TGTTCATCTCTTCATGACCTGCTCACTGCTGAGAGGATATGGCTCATCTGTAACCC 540
 QY 590 ATGGGGCACTCCAGAAAGGCAAACTTGGCATTTGCTTCCCTGGCAATATGCTG 649
 DB 541 ATGGGGCACTCCAGAAAGGCAAACTTGGCATTTGCTTCCCTGGCAATATGCTG 600
 QY 650 CTGACTCTGCTGTCACCATCTCTTTTATATGTCGTAAGCAACATCTTCACTCTG 709
 DB 601 CTGACTCTGCTGTCACCATCTCTTTTATATGTCGTAAGCAACATCTTCACTCTG 660
 QY 710 CTGAACATGACGACCTGTCATGATGTTTGCCTGAGAGAGCTCTTGGTGGAGACATGTC 769
 DB 661 CTGAACATGACGACCTGTCATGATGTTTGCCTGAGAGAGCTCTTGGTGGAGACATGTC 720
 QY 770 AATTACTTCTCTCTCTGCGCATTTGGGATCTTTCTGTTCCAGCTTCTCAAGCTCT 829
 DB 721 AATTACTTCTCTCTCTGCGCATTTGGGATCTTTCTGTTCCAGCTTCTCAAGCTCT 780
 QY 830 GCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 889
 DB 781 GCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 890 AAAAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 949
 DB 841 AAAAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900

QY	950	CTCCTAGTAAACCTTCAGCTGTGTGTGATTAATTTGATTAAGACCAAGGCAAGC	1009
QY <td>901</td> <td>ACTCCTAGTAAACCTTCAGCTGTGTGTGATTAATTTGATTAAGACCAAGGCAAGC</td> <td>960</td>	901	ACTCCTAGTAAACCTTCAGCTGTGTGTGATTAATTTGATTAAGACCAAGGCAAGC	960
QY <td>1010</td> <td>CATGTCATAGCCCTGTACATTTGATTCAGCTGTACCTTAAACAGCTGCATGCAC</td> <td>1069</td>	1010	CATGTCATAGCCCTGTACATTTGATTCAGCTGTACCTTAAACAGCTGCATGCAC	1069
Db <td>961</td> <td>CATGTCATAGCCCTGTACATTTGATTCAGCTGTACCTTAAACAGCTGCATGCAC</td> <td>1020</td>	961	CATGTCATAGCCCTGTACATTTGATTCAGCTGTACCTTAAACAGCTGCATGCAC	1020
QY <td>1070</td> <td>CCCTTTGTCATTAATTTGTTTCAATATTTCAAGGATTCATGCAAGAAAGAGCTCTCCTT</td> <td>1129</td>	1070	CCCTTTGTCATTAATTTGTTTCAATATTTCAAGGATTCATGCAAGAAAGAGCTCTCCTT	1129
Db <td>1021</td> <td>CCCTTTGTCATTAATTTGTTTCAATATTTCAAGGATTCATGCAAGAAAGAGCTCTCCTT</td> <td>1080</td>	1021	CCCTTTGTCATTAATTTGTTTCAATATTTCAAGGATTCATGCAAGAAAGAGCTCTCCTT	1080
QY <td>1130</td> <td>TGCCGAAAGTCCGCACTGTAAAGCAGATGCAAGTACCCCTCACCTCAAAAGAAACATCC</td> <td>1189</td>	1130	TGCCGAAAGTCCGCACTGTAAAGCAGATGCAAGTACCCCTCACCTCAAAAGAAACATCC	1189
Db <td>1081</td> <td>TGCCGAAAGTCCGCACTGTAAAGCAGATGCAAGTACCCCTCACCTCAAAAGAAACATCC</td> <td>1140</td>	1081	TGCCGAAAGTCCGCACTGTAAAGCAGATGCAAGTACCCCTCACCTCAAAAGAAACATCC	1140
QY <td>1190</td> <td>AGGAATTCACACTCTTACTCTTCAAGTTCAACCACTGTAAAGACCTCCTATTGA</td> <td>1243</td>	1190	AGGAATTCACACTCTTACTCTTCAAGTTCAACCACTGTAAAGACCTCCTATTGA	1243
Db <td>1141</td> <td>AGGAATTCACACTCTTACTCTTCAAGTTCAACCACTGTAAAGACCTCCTATTGA</td> <td>1194</td>	1141	AGGAATTCACACTCTTACTCTTCAAGTTCAACCACTGTAAAGACCTCCTATTGA	1194

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RESULT 15
AA084558
ID AA084558 standard; DNA; 1255 BP.
XX
XX AC AA084558;
XX
XX DT 25-MAR-2003 (revised)
XX DT 22-AUG-1995 (first entry)
XX DB Human C140 receptor genomic DNA.
XX
XX KW G-protein-coupled receptor; G-protein; C140 receptor; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 56..1197
XX FT /*tag= a
XX
XX MN WO9503318-A1.
XX
XX PD 02-FEB-1995.
XX
XX PF 26-JUL-1994; 94WO-US008536.
XX
XX PR 26-JUL-1993; 93US-00097938.
XX
XX PA (CORT-) COR THERAPEUTICS.
XX
XX SC Scarborough RM, Sundelin J;
XX PI WPI, 1995-075182/10.
XX DR P-PSDB; AAR66521.
XX
XX PT New DNA encoding recombinant C140 receptor - and novel agonists and
XX PT antagonists and specific antibodies with therapeutic and diagnostic
XX PT applications.
XX
XX XX Disclosure; Fig 2; 57pp; English.
XX
XX The availability of genomic DNA encoding the mouse protease C140 receptor
XX (see Q84557) permitted the retrieval of the corresp. human gene. A human
XX genomic library cloned in the vector EMB3 was screened using the entire
XX coding region of the murine clone as a probe. The recovered human gene
XX including the DNA sequence and the deduced AA sequence are shown in
XX Q84558 & R66921. Subsequent experiments indicated that the human C140
XX gene is located in the same region of the long arm of chromosome number 5
XX (5q12-5q13) as has been reported for the human thrombin receptor gene.
XX *(Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 1255 BP; 294 A; 320 C; 260 G; 381 T; 0 U; 0 Other;

```

Query Match	78.2%	Score 1105.8	DB 2	Length 1255	
Beet Local Similarity	99.4%	Pred. No. 0			
Matches 1110	Conservative	0	Mismatches	7	Indels
		0	Gaps	0	
QY	130	AGGAACCAATGATCCTCTAAAGGAAGACCTTATGGTAAGGTGATGCAATCCCA	189		
DB	139	AGGAACCAATGATCCTCTAAAGGAAGACCTTATGGTAAGGTGATGCAATCCCA	198		
QY	190	CGTCACTGGAAGAAGATTACAGTTGAAACAGTCTTTCTGTGATGAGTTTCTGCATC	249		
DB	199	CGTCACTGGAAGAAGAGATTACAGTTGAAACAGTCTTTCTGTGATGAGTTTCTGCATC	258		
QY	250	TGTCTCGCTGGAAGAACGACCACTGTCTTCCCATTTGTCACAAATGTGTTGC	309		
DB	259	TGTCTCTCACTGGAAGAACGACCACTGTCTTCCCATTTGTCACAAATGTGTTGT	318		
QY	310	GGTGGGTTTGGCCAAGTAAACGGCAATGCGCTTATGGGTCTTTCTTTCCGAACTAAGAGAA	369		
DB	319	GGTGGGTTTGGCCAAGTAAACGGCAATGCGCTTATGGGTCTTTCTTTCCGAACTAAGAGAA	378		
QY	370	GCACCTGTGTGATTTACATGCGCAATCTGGCCTTGGCTGACCTCTCTGTGATCTG	429		
DB	379	GCACCTGTGTGATTTACATGCGCAATCTGGCCTTGGCTGACCTCTCTGTGATCTG	438		
QY	430	GTTCCCTCTGGAAGATGGCTTACATACATGAGCAACAACGGAATTATGGGGAAAGCTC	489		
DB	439	GTTCCCTCTGGAAGATGGCTTACATACATGAGCAACAACGGAATTATGGGGAAAGCTC	498		
QY	490	TTGTAAATGTGCTATTTGGCTTTTCTATCGCAACATGATCGTTCATTTCTTCATGAC	549		
DB	499	TTGTAAATGTGCTATTTGGCTTTTCTATCGCAACATGATCGTTCATTTCTTCATGAC	558		
QY	550	CTGCCTCAGTGTGAGAGTAAATTTGGGTCAATGTGAACCCCAATGGGGCACTCCAGAGAA	609		
DB	559	CTGCCTCAGTGTGAGAGTAAATTTGGGTCAATGTGAACCCCAATGGGGCACTCCAGAGAA	618		
QY	610	GGCAAACTTTGCCATTTGGCATCTCCCTGGCAATAATGCTGTGACTCTGCTGTGTCA	669		
DB	619	GGCAAACTTTGCCATTTGGCATCTCCCTGGCAATAATGCTGTGACTCTGCTGTGTCA	678		
QY	670	CCCTTTGATATGCGTGAAGACAGACATCTTCATTCCTGACCCTGAACATCAACA	729		
DB	679	CCCTTTGATATGCGTGAAGACAGACATCTTCATTCCTGACCCTGAACATCAACA	738		
QY	730	TGATGTTTGGCTGAGCAGCTCTTGATGGGAGACATGTTCAATTACTTCTCTCTGGC	789		
DB	739	TGATGTTTGGCTGAGCAGCTCTTGATGGGAGACATGTTCAATTACTTCTCTCTGGC	798		
QY	790	CATTGGGGTCTTTCTGTTCCCAAGCTTCTCAACGCTCTGCTATGTGTGATGATCAG	849		
DB	799	CATTGGGGTCTTTCTGTTCCCAAGCTTCTCAACGCTCTGCTATGTGTGATGATCAG	858		
QY	850	AATGTGTGATCTTCTGCGCATGATGTAATACTCAGAGAAAGAAAGAGAGGGCATCAA	909		
DB	859	AATGTGTGATCTTCTGCGCATGATGTAATACTCAGAGAAAGAAAGAGAGGGCATCAA	918		
QY	910	ACTCATGTGACTGTCTGCGCATGATGTAACCTGATCTGCTTCACTCTGATGATCCTTCTGCT	969		
DB	919	ACTCATGTGACTGTCTGCGCATGATGTAACCTGATCTGCTTCACTCTGATGATCCTTCTGCT	978		
QY	970	TGTGGTGCAATATTTCTGATTTAAGACAGGGCCAGACAGCATGTCTAATGCTGTGAT	1029		
DB	979	TGTGGTGCAATATTTCTGATTTAAGACAGGGCCAGACAGCATGTCTAATGCTGTGAT	1038		
QY	1030	TGTAGCCCTGTGCTCTCTCAACCTTAAACGTGTGATGACCCCTTTGTCTATTA	1089		
DB	1039	TGTAGCCCTGTGCTCTCTCTCAACCTTAAACGTGTGATGACCCCTTTGTCTATTA	1098		
QY	1090	TTTCACTATGATTTCAAGGATCATGCAAGAAACGCTCTCCCTTTCGGAAGTGTCCGCACTGT	1149		
DB	1099	TTTCACTATGATTTCAAGGATCATGCAAGAAACGCTCTCCCTTTCGGAAGTGTCCGCACTGT	1158		
QY	1150	AAAGCAATGCAAGTACCCCTCACTCATTAAGAAACACTCCAGAAATTCAGCTCTTA	1209		

Db	1159	AAAGCAGATGCAGTAATCCCTCAGCTCAAGAAACACTCCAGGAAATCCAGCTTACTC	1218
Qy	1210	TTCAAGTTCAACCACTGTTAAAGCTTCCTATTGAGTT	1246
Db	1219	TTCAAGTTCAACCACTGTTAAAGCTTCCTATTGAGTT	1255

Search completed: March 21, 2005, 18:18:56
Job time : 830.407 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2005, 20:59:39 ; Search time 68.9132 Seconds
(without alignments)
2228.076 Million cell updates/sec

Title: US-10-643-627-63
Perfect score: 2031
Sequence: 1 MRSPPSAWMLGAAILAASL.....KHSRKSSSYSSSTVTKTSY 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2023	99.6	397	2 AAR66923	AAR66923 Human C14
2	2023	99.6	397	2 AAW01955	AAW01955 Human C14
3	2003	98.6	397	3 AAB35641	AAB35641 Human PAR
4	2003	98.6	397	5 AAE26678	AAE26678 Human coa
5	2003	98.6	397	6 ABG73508	ABG73508 Human par
6	2003	98.6	397	7 ADE62812	ADE62812 Human pro
7	2003	98.6	397	8 ADO29311	ADO29311 Human GPC
8	2003	98.6	397	8 AD574020	AD574020 Human G-P
9	1998	98.4	397	8 ADL61221	ADL61221 Human coa
10	1997	98.3	397	6 ABP81907	ABP81907 Human pro
11	1997	98.3	397	7 ADK52594	ADK52594 Hematolog
12	1997	98.3	397	7 ADN39997	ADN39997 Cancer/an
13	1997	98.3	397	8 ADR46675	ADR46675 Cancer-as
14	1965.5	96.8	394	2 AAW51408	AAW51408 Human pro
15	1884.5	92.8	398	8 ADO28601	ADO28601 Human PAR
16	1880	92.6	398	2 AAR65921	AAR65921 Human C14
17	1880	92.6	398	2 AAW01953	AAW01953 Human C14
18	1793	88.3	355	8 ADI28653	ADI28653 Human mod
19	1720	84.7	341	8 ADI28654	ADI28654 Human mod
20	1713	84.3	399	2 AAR66922	AAR66922 Murine C1
21	1713	84.3	399	2 AAW01954	AAW01954 Murine C1
22	1713	84.3	399	7 ABR63562	ABR63562 Delayed h
23	1707	84.0	397	7 ADE62810	ADE62810 Rat Prote
24	1644.5	81.0	395	2 AAR66920	AAR66920 Murine C1

26	1639.5	80.7	395	2 AAW01952	AAW01952 Murine C1
27	1625	80.0	320	8 ADI28655	ADI28655 Human mod
28	611	30.1	420	6 ABG73510	ABG73510 X. laevis
29	609	30.0	430	8 ADO29310	ADO29310 Mouse GPC
30	608	29.9	425	2 AAR27240	AAR27240 Human chr
31	608	29.9	425	2 AAR60698	AAR60698 Fragment
32	608	29.9	425	2 AAW51407	AAW51407 Human pro
33	608	29.9	425	2 AAY49570	AAY49570 Human chr
34	608	29.9	425	5 AAR17032	AAR17032 Novel hum
35	608	29.9	425	5 AAG80697	AAG80697 Human chr
36	608	29.9	425	6 ABG73511	ABG73511 Human chr
37	608	29.9	425	6 ABR47449	ABR47449 Breat ca
38	608	29.9	425	6 ABP81919	ABP81919 Human chr
39	608	29.9	425	7 ADG89876	ADG89876 Human coa
40	608	29.9	425	8 ADL14208	ADL14208 Novel hum
41	608	29.9	425	8 ADN04016	ADN04016 Antiporci
42	608	29.9	425	8 ADO29309	ADO29309 Human sof
43	608	29.9	425	8 ADQ18985	ADQ18985 Human GPC
44	608	29.9	425	8 ADR45608	ADR45608 Human G P
45	608	29.9	425	8 ADS84489	ADS84489 Human pro

ALIGNMENTS

RESULT 1
ID AAR66923 standard; protein; 397 AA.
XX
AC AAR66923;
XX
DT 25-MAR-2003 (revised)
DT 22-AUG-1995 (first entry)
XX
DE Human C140 receptor encoded by cDNA.
XX
KM G-protein-coupled receptor; G-protein; C140 receptor.
XX
OS Homo sapiens.
XX
PN WO9503318-A1.
XX
PD 02-FEB-1995.
XX
PP 26-JUL-1994; 94MO-US008536.
XX
PR 26-JUL-1993; 93US-00097938.
XX
PA (COR-) COR THERAPEUTICS.
PI Scarborough RM, Sundelin J;
XX
XX WPI; 1995-075182/10.
DR N-FSDB; AAQ84560.
XX
PT New DNA encoding recombinant C140 receptor - and novel agonists and
PT antagonists and specific antibodies with therapeutic and diagnostic
PT applications.
PS
XX Example; Fig 11; 57pp; English.
CC A human intestinal tumour cDNA library was subjected to PCR using primers
CC designed from the genomic clone (see AAQ84558) and the amplified fragment
CC was cloned in pSG5 and sequenced. There are four AA differences between
CC the cDNA encoded sequence and that encoded by the genomic DNA. The
CC genomic DNA sequence and deduced AA sequence are given in AAQ84560 &
CC AAR66923. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 397 AA;
Query Match 99.6%; Score 2023; DB 2; Length 397;
Best Local Similarity 99.7%; Pred. No. 1.1e-210;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MESPSPAAWMLLGAAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGTSHTGKGVTVETVS 60
DB 1 MESPSPAAWMLLGAAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGTSHTGKGVTVETVS 60
QY 61 VDEFSASVLAGKLTVPPIVYTIYPAVGLPSNGMALWFLPRTKKKHPAVIYMANLALA 120
DB 61 VDEFSASVLAGKLTVPPIVYTIYPAVGLPSNGMALWFLPRTKKKHPAVIYMANLALA 120
QY 121 DLLSVWPFPLKIAHYHNGNMWYGEALCNVLIGFFYGNMYCSILFMTCLSVORWYIYVP 180
DB 121 DLLSVWPFPLKIAHYHNGNMWYGEALCNVLIGFFYGNMYCSILFMTCLSVORWYIYVP 180
QY 181 MGHSRKKANIAIGISLAIWMLTLVTPIDYVVKQTIFIPALNITTCGDVLPBQLLVGDMF 240
DB 181 MGHSRKKANIAIGISLAIWMLTLVTPIDYVVKQTIFIPALNITTCGDVLPBQLLVGDMF 240
QY 241 NYFLSLAIGVFLPAPALTASAVYLMIRMLRSSAMDBNSKRRRAIKLIVTVLGMVLICF 300
DB 241 NYFLSLAIGVFLPAPALTASAVYLMIRMLRSSAMDBNSKRRRAIKLIVTVLGMVLICF 300
QY 301 TSPNLLLVVHYFLIKSQGSHVYALYVALCLSTLNSCIDPFVYVYFVSHDFRDHAKNAL 360
DB 301 TSPNLLLVVHYFLIKSQGSHVYALYVALCLSTLNSCIDPFVYVYFVSHDFRDHAKNAL 360
QY 361 CRSVRTVKOMQVPLTSKGRSSSYSSSTTVKTSY 397
DB 361 CRSVRTVKOMQVPLTSKGRSSSYSSSTTVKTSY 397

```

RESULT 2

AAW01955
ID AAW01955 standard; protein; 397 AA.

AC AAW01955;

DT 02-APR-1997 (first entry)

XX Human C140 receptor.

XX C140 receptor; G-protein linked; coupled; seven pass; agonist;

XX antagonist; hypertension; hypotension; blood pressure.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..27 /note="the signal peptide differs from that encoded by a

FT genomic DNA sequence for this receptor (see AAW01953),

FT the signal sequence given here is believed to be the

FT correct sequence"

FT Protein 28..397 /note="mature protein"

XX MO9623225-A1.

XX 01-AUG-1996.

XX 25-JAN-1996; 96MO-US001179.

XX 25-JAN-1995; 95US-00390301.

XX (CORT-) COR THERAPEUTICS INC.

XX Sundelin J, Scarborough RM;

XX WPI; 1996-362813/36.

XX DR N-PSDB; AAT32039.

XX Vector for expression C140 cell surface receptor in host cell - useful to

XX identify C140 agonist and antagonists, which are antihypertensives and

XX PT elevators of blood pressure, respectively.

PS Example 5; Fig 11A-B; 60pp; English.

XX AAW01955 represents the human C140 receptor (C140R). DNA encoding C140R

CC may be engineered so as to allow the recombinant expression of C140R in a

CC suitable host cell, i.e. by removing the native expression-control

CC sequences and replacing them with control sequences operable in the host.

CC Such a recombinant receptor can be expressed on the surface of oocytes, of

CC this provides a good assay system for identifying agonists/antagonists of

CC the "seven-pass" transmembrane receptor superfamily (peptide chain of the

CC receptor passes through the cell membrane seven times, producing seven

CC transmembrane regions within the receptor molecule). The C140 receptor is

CC involved in controlling blood pressure. C140 antagonists (see AAW01942,

CC an increase in blood pressure and are therefore useful in pharmaceuticals

CC for the treatment of hypertension (low blood pressure). Conversely

CC agonists (see AAW01944-W01941) of C140 are useful in pharmaceuticals for

CC the treatment of hypertension (high blood pressure)

CC

SQ Sequence 397 AA;

Query Match 99.6%; Score 2023; DB 2; Length 397;

Best Local Similarity 99.7%; Pred. No. 1..le-210;

Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESPSPAAWMLLGAAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGTSHTGKGVTVETVS 60

DB 1 MESPSPAAWMLLGAAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGTSHTGKGVTVETVS 60

QY 61 VDEFSASVLAGKLTVPPIVYTIYPAVGLPSNGMALWFLPRTKKKHPAVIYMANLALA 120

DB 61 VDEFSASVLAGKLTVPPIVYTIYPAVGLPSNGMALWFLPRTKKKHPAVIYMANLALA 120

QY 121 DLLSVWPFPLKIAHYHNGNMWYGEALCNVLIGFFYGNMYCSILFMTCLSVORWYIYVP 180

DB 121 DLLSVWPFPLKIAHYHNGNMWYGEALCNVLIGFFYGNMYCSILFMTCLSVORWYIYVP 180

QY 181 MGHSRKKANIAIGISLAIWMLTLVTPIDYVVKQTIFIPALNITTCGDVLPBQLLVGDMF 240

DB 181 MGHSRKKANIAIGISLAIWMLTLVTPIDYVVKQTIFIPALNITTCGDVLPBQLLVGDMF 240

QY 241 NYFLSLAIGVFLPAPALTASAVYLMIRMLRSSAMDBNSKRRRAIKLIVTVLGMVLICF 300

DB 241 NYFLSLAIGVFLPAPALTASAVYLMIRMLRSSAMDBNSKRRRAIKLIVTVLGMVLICF 300

QY 301 TSPNLLLVVHYFLIKSQGSHVYALYVALCLSTLNSCIDPFVYVYFVSHDFRDHAKNAL 360

DB 301 TSPNLLLVVHYFLIKSQGSHVYALYVALCLSTLNSCIDPFVYVYFVSHDFRDHAKNAL 360

QY 361 CRSVRTVKOMQVPLTSKGRSSSYSSSTTVKTSY 397

DB 361 CRSVRTVKOMQVPLTSKGRSSSYSSSTTVKTSY 397

RESULT 3

AAAB35641
ID AAB35641 standard; protein; 397 AA.

XX AAB35641;

XX 19-FEB-2001 (first entry)

XX Human PAR-2 protein.

XX PAR-2; protease activated receptor-2; ECL-2; inflammatory disease;

XX asthma; chronic obstructive pulmonary; arthritis; inflammatory bowel;

XX psoriasis; eczema; multiple sclerosis.

XX Homo sapiens.

XX MO200063371-A1.

XX 26-OCT-2000.

XX 17-APR-2000; 2000MO-GB001455.
 XX 15-APR-1999; 99GB-00008513.
 XX (UYSC-) UNIV SOUTHAMPTON.
 XX Wallis AF, Palmer K, Compton SJ, Cairns JA, Gough AC;
 XX WPI, 2000-679599/66.
 XX
 XX Protease activated receptor 2 variants useful for treating inflammatory
 XX diseases such as asthma, arthritis and psoriasis, and as hypertensives,
 XX has reduced sensitivity to trypsin.
 XX
 XX Claim 2; Page 55; 59pp; English.
 XX
 XX The present invention relates to a variant protease activated receptor 2
 XX (PAR-2). The invention is useful for identifying an individual having a
 XX polymorphism in the ECL-2 region of one or both PAR-2 gene alleles. The
 XX invention may be used to develop treatments for inflammatory diseases
 XX such as asthma, chronic obstructive pulmonary diseases, arthritis,
 XX inflammatory bowel diseases, psoriasis and eczema, multiple sclerosis and
 XX to raise blood pressure
 XX
 XX Sequence 397 AA;

Query Match 98.6%; Score 2003; DB 3; Length 397;
 Best Local Similarity 98.7%; Pred. No. 1,7e-208;
 Matches 392; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRSPSAAMLGAAILLAASISCSGTTGTRRSKGRSLGKVDGTSHTGKGVTVETVFS 60
 DB 1 MRSPSAAMLGAAILLAASISCSGTTGTRRSKGRSLGKVDGTSHTGKGVTVETVFS 60
 QY 61 VDEFSASVLAGKLTTFVLPVYTVIVAVGLPSNGMALWVFLPRTKKGHPAVIYMANIALA 120
 DB 61 VDEFSASVLAGKLTTFVLPVYTVIVAVGLPSNGMALWVFLPRTKKGHPAVIYMANIALA 120
 QY 121 DLLSVIWPPLKIAHYIHGNMVIYGBALCNVLIGFFGNMYSILFMTCLSVGRYWIYVNP 180
 DB 121 DLLSVIWPPLKIAHYIHGNMVIYGBALCNVLIGFFGNMYSILFMTCLSVGRYWIYVNP 180
 QY 121 DLLSVIWPPLKIAHYIHGNMVIYGBALCNVLIGFFGNMYSILFMTCLSVGRYWIYVNP 180
 DB 121 DLLSVIWPPLKIAHYIHGNMVIYGBALCNVLIGFFGNMYSILFMTCLSVGRYWIYVNP 180
 QY 181 MGRSRKANAIAGISLAIWLLTLVTPLYVVKQTIFIPALNTTCHDVLPBOLLVGDMF 240
 DB 181 MGRSRKANAIAGISLAIWLLTLVTPLYVVKQTIFIPALNTTCHDVLPBOLLVGDMF 240
 QY 241 NYFLSLAIGVFLPPAFLTASAVYLMIRLSSAMDENSEKKRAIKLIVTVGMYLICF 300
 DB 241 NYFLSLAIGVFLPPAFLTASAVYLMIRLSSAMDENSEKKRAIKLIVTVGMYLICF 300
 QY 301 TSPNLLIVHYPLIKSGQSHVYALVVALCLSTLNSCIDPFFVYFVSHDFRDHAKNALL 360
 DB 301 TSPNLLIVHYPLIKSGQSHVYALVVALCLSTLNSCIDPFFVYFVSHDFRDHAKNALL 360
 QY 361 CRSVRITKQWQVPLTSKGRSKSSVSSSTTYKTSY 397
 DB 361 CRSVRITKQWQVPLTSKGRSKSSVSSSTTYKTSY 397

RESULT 4
 AAB26678
 ID AAB26678 standard, protein; 397 AA.

XX AAB26678;
 XX DT 13-DEC-2002 (first entry)
 XX
 XX Human coagulation factor II (thrombin) receptor like 1 (F2RL1) protein.
 XX Human; haplotype; coagulation factor II receptor like 1; F2RL1; asthma;
 XX polymorphism; chronic pulmonary disease; inflammatory disorder;
 XX gene therapy.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 30
 FT /note= "This amino acid changes to Ser due to single
 FT nucleotide polymorphism"
 XX
 XX WO20025534-A2.
 XX
 XX 18-JUL-2002.
 XX
 XX 13-NOV-2001; 2001MO-US046475.
 XX
 XX 10-NOV-2000; 2000US-0247516P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Blegleckl KM, Sanchis A, Shah N;
 XX WPI, 2002-566728/60.
 XX N-PSDB; AAD44437, AAD44438.
 XX
 XX New genetic variants having polymorphisms in the coagulation factor II
 XX (thrombin) receptor like 1 (F2RL1) gene, useful for studying the function
 XX of F2RL1 and treating disorders associated with abnormal expression or
 XX function of F2RL1.
 XX
 XX Claim 27; Fig 3; 65pp; English.

XX The invention relates to an isolated polynucleotide comprising genes and
 XX haplotypes of the coagulation factor II (thrombin) receptor like 1
 XX (F2RL1) gene. Polymorphic variants of the F2RL1 gene are useful in
 XX studying the expression and biological function of F2RL1, and in
 XX identifying drugs targeting F2RL1 protein for treating disorders
 XX associated with abnormal expression or function of F2RL1, e.g. asthma,
 XX chronic pulmonary disease, and inflammatory disorders. Polynucleotides
 XX comprising a polymorphic gene variant or fragment may be used for
 XX therapeutic purposes, where a patient could benefit from expression or
 XX increased expression of a particular F2RL1 protein isoform, or an
 XX expression vector encoding the isoform may be administered to the
 XX patient. Haplotype information is useful in improving the efficiency and
 XX output of several steps in drug discovery and development process,
 XX including target validation, identifying lead compounds, and early phase
 XX clinical trials. Information on polymorphisms may be applied in studying
 XX biological functions of F2RL1 as well as in identifying drugs targeting
 XX this protein for the treatment of disorders related to its abnormal
 XX expression or function. The invention is useful in gene therapy. The
 XX present sequence is human F2RL1 protein

Query Match 98.6%; Score 2003; DB 5; Length 397;
 Best Local Similarity 98.7%; Pred. No. 1,7e-208;
 Matches 392; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRSPSAAMLGAAILLAASISCSGTTGTRRSKGRSLGKVDGTSHTGKGVTVETVFS 60
 DB 1 MRSPSAAMLGAAILLAASISCSGTTGTRRSKGRSLGKVDGTSHTGKGVTVETVFS 60
 QY 61 VDEFSASVLAGKLTTFVLPVYTVIVAVGLPSNGMALWVFLPRTKKGHPAVIYMANIALA 120
 DB 61 VDEFSASVLAGKLTTFVLPVYTVIVAVGLPSNGMALWVFLPRTKKGHPAVIYMANIALA 120
 QY 121 DLLSVIWPPLKIAHYIHGNMVIYGBALCNVLIGFFGNMYSILFMTCLSVGRYWIYVNP 180
 DB 121 DLLSVIWPPLKIAHYIHGNMVIYGBALCNVLIGFFGNMYSILFMTCLSVGRYWIYVNP 180
 QY 181 MGRSRKANAIAGISLAIWLLTLVTPLYVVKQTIFIPALNTTCHDVLPBOLLVGDMF 240
 DB 181 MGRSRKANAIAGISLAIWLLTLVTPLYVVKQTIFIPALNTTCHDVLPBOLLVGDMF 240
 QY 241 NYFLSLAIGVFLPPAFLTASAVYLMIRLSSAMDENSEKKRAIKLIVTVGMYLICF 300
 DB 241 NYFLSLAIGVFLPPAFLTASAVYLMIRLSSAMDENSEKKRAIKLIVTVGMYLICF 300

DB 241 NYFLSLAIGVFLPAPALTASAYVLMIRMLRSSAMDNSEKKRAIKLIVTVLAMYLCF 300
QY 301 TTSNLLLVVHYFLIKSQGSHVYALYVALCISTLNSCIDPFYVYVSHDFRDHAKNALL 360
DB 301 TTSNLLLVVHYFLIKSQGSHVYALYVALCISTLNSCIDPFYVYVSHDFRDHAKNALL 360
QY 361 CRSVRTVKOMQVPLTSKSKSRKSSSYSSSTTVKTSY 397
DB 361 CRSVRTVKOMQVPLTSKSKSRKSSSYSSSTTVKTSY 397

RESULT 5
ABG73508
ID ABG73508 standard; protein; 397 AA.
XX
XX ABG73508;
AC
XX
XX 14-FEB-2003 (first entry)
XX
XX
DE Human par2 protein SEQ ID 39.
XX
XX
XX G-protein coupled receptor; HGPBMY1, HGPBMY2; immunosuppressive;
XX cardiant; neuroprotective; antiinflammatory; cyostatic; vulnary;
XX vaccine; gene therapy; autoimmune; cardiovascular; neural; reproductive;
XX haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
XX birth defect; aberrant phosphorylation; acute phase response; receptor;
XX signal transduction; hyperimmune activity; inflammatory; hypercongenital;
XX necrotic lesion; wound; organ transplant rejection.
XX
XX Homo sapiens.
XX
XX MO200268591-A2.
XX
XX
XX 06-SEP-2002.
XX
XX 22-FEB-2002; 2002WO-US005281.
XX
XX 23-FEB-2001; 2001US-0270792P.
XX 23-FEB-2001; 2001US-0270793P.
XX 06-JUN-2001; 2001US-0296427P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX
XX Feder J, Ramathan C, Nelson T, Mintier G, Cacace A, Barber L;
XX Kornacker M, Bol D;
XX MPI, 2003-058304/05.
XX
XX
XX New human HGPBMY1 or HGPBMY2 polynucleotide and polypeptide, useful
XX preventing, treating or ameliorating a disorder e.g., wound,
XX cardiovascular disorder or transplant rejection.
XX
XX Disclosure; Fig 4; 316pp; English.
XX
XX
XX This invention describes the novel human G-protein coupled receptors
XX (GPCR's), HGPBMY1 or HGPBMY2 which have immunosuppressive, cardiant,
XX neuroprotective, antiinflammatory, cyostatic and vulnary activity and
XX can be used in vaccines or for gene therapy. Pharmaceutical compositions
XX comprising HGPBMY1 or HGPBMY2 polypeptides or their agonists or
XX antagonists or modulators, or a HGPBMY1- or HGPBMY2-specific antibody
XX are useful for preventing, treating or ameliorating a medical condition
XX comprising autoimmune, cardiovascular, neural, reproductive,
XX haematopoietic, pulmonary, gastrointestinal or proliferating disorder, a
XX cell cycle or birth defect, a disorder related to aberrant
XX phosphorylation, acute phase responses or signal transduction or to
XX hyperimmune activity, an inflammatory or hypercongenital condition, a
XX necrotic lesion, a wound, organ transplant rejection or a condition
XX related to organ transplant rejection. This sequence represents a G-
XX protein coupled receptor associated with the human HGPBMY proteins
XX described in the disclosure of the invention
XX
XX Sequence 397 AA;

Query Match 98.6%; Score 2003; DB 6; Length 397;
Best Local Similarity 98.7%; Pred. No. 1.7e-208;
Matches 392; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 MNSPSAAMLLGAAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
DB 1 MNSPSAAMLLGAAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
QY 61 VDEFSASVLAGLITVFLPIVTVIVPAVGLPSNGMALMYFLFRITKGGPAVIYMANLALA 120
DB 61 VDEFSASVLAGLITVFLPIVTVIVPAVGLPSNGMALMYFLFRITKGGPAVIYMANLALA 120
QY 121 DILSVIWPFLKIAVHIGNNMITYGALCNVLIGFPYNNYCSILFWTCISVORRYWYVNP 180
DB 121 DILSVIWPFLKIAVHIGNNMITYGALCNVLIGFPYNNYCSILFWTCISVORRYWYVNP 180
QY 181 MGHSRKKANIAIGISLAIWLLTLVTIPIYVVKQITFIIPALNITTCDDVLPQDLVGDNF 240
DB 181 MGHSRKKANIAIGISLAIWLLTLVTIPIYVVKQITFIIPALNITTCDDVLPQDLVGDNF 240
QY 241 NYFLSLAIGVFLPAPALTASAYVLMIRMLRSSAMDNSEKKRAIKLIVTVLAMYLCF 300
DB 241 NYFLSLAIGVFLPAPALTASAYVLMIRMLRSSAMDNSEKKRAIKLIVTVLAMYLCF 300
QY 301 TTSNLLLVVHYFLIKSQGSHVYALYVALCISTLNSCIDPFYVYVSHDFRDHAKNALL 360
DB 301 TTSNLLLVVHYFLIKSQGSHVYALYVALCISTLNSCIDPFYVYVSHDFRDHAKNALL 360
QY 361 CRSVRTVKOMQVPLTSKSKSRKSSSYSSSTTVKTSY 397
DB 361 CRSVRTVKOMQVPLTSKSKSRKSSSYSSSTTVKTSY 397

RESULT 6
ADE62812
ID ADE62812 standard; protein; 397 AA.
XX
XX
XX ADE62812;
AC
XX
XX 29-JUN-2004 (first entry)
XX
XX
XX Human Protein P55085, SEQ ID NO 8745.
XX
XX
XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNr; Chung.
XX
XX Homo sapiens.
XX
XX
XX MO2003016475-A2.
XX
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX MPI, 2003-268312/26.
XX GENBANK; P55085.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 397 AA;

XX Query Match 98.6%; Score 2003; DB 7; Length 397;

XX Best Local Similarity 98.7%; Pred. No. 1.7e-208; Matches 397; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

XX 1 MRSPSAAMLGAAILLAASISCGTIGTRSSKGRSLIGKVDGTSHTVGKVTETVFS 60
 DB 1 MRSPSAAMLGAAILLAASISCGTIGTRSSKGRSLIGKVDGTSHTVGKVTETVFS 60
 QY 61 VDBPSASVLAGKTTTTPVTVTVPAVGLPSCNMLMWPLFRKKGHPAVIYMANALA 120
 DB 61 VDBPSASVLAGKTTTTPVTVTVPAVGLPSCNMLMWPLFRKKGHPAVIYMANALA 120
 QY 121 DLISVIMFPLKIAVHIGNMVIGALCNVLIQFPYGMVCSILFMTCLSVORWVAVNP 180
 DB 121 DLISVIMFPLKIAVHIGNMVIGALCNVLIQFPYGMVCSILFMTCLSVORWVAVNP 180
 QY 181 MGSRRKANAIAGISLAIMLTLLVTIPLVYVQGTIPALNITTCDDVLPBQLLVGDMF 240
 DB 181 MGSRRKANAIAGISLAIMLTLLVTIPLVYVQGTIPALNITTCDDVLPBQLLVGDMF 240
 QY 241 NYPLSLAIGVPLPPAFTASAYTLMIMLASSANDSEKKRKAICLYTVVLCMYLICF 300
 DB 241 NYPLSLAIGVPLPPAFTASAYTLMIMLASSANDSEKKRKAICLYTVVLCMYLICF 300
 QY 301 TPNLNLVHYVPLIKSGQSGSHVVALYVVALCLSTLNSCIDPPVYFVPSHDPBDHAKNAL 360
 DB 301 TPNLNLVHYVPLIKSGQSGSHVVALYVVALCLSTLNSCIDPPVYFVPSHDPBDHAKNAL 360
 QY 361 CRGVRVTKQVQVPLTSKGSRRKSSVSSSTTVVTSY 397
 DB 361 CRGVRVTKQVQVPLTSKGSRRKSSVSSSTTVVTSY 397

XX RESULT 7
 XX ADO29311 standard; protein; 397 AA.

XX ADO29311;

XX 79-JUL-2004 (first entry)

XX Human GPCR F2RL1, SEQ ID NO:412.

KM G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KM transgenic mouse; neurological disorder; adrenal gland disorder;
 KM colon disorder; intestinal disorder; cardiovascular disorder;
 KM muscular disorder; blood disorder; immune disorder; bone disorder;
 KM joint disorder; metabolic disorder; nutritive disorder; cancer;
 KM kidney disorder; liver disorder; lung disorder; breast disorder;
 KM ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KM skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KM thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;
 KM cytostatic; antineoplastic; vasotropic; antidiabetic;
 KM CNS; central nervous system; respiratory; antidiabetic;
 KM virucide; hepatotropic; antibacterial; antineoplastic; antidiabetic;
 KM dermatological; antitumor; antihypertensive; anorectic;
 KM immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;
 KM receptor.
 XX Homo sapiens.
 OS WO2004040000-A2.
 XX 13-MAY-2004.
 PD 09-SEP-2003; 2003WO-US028226.
 XX 09-SEP-2002; 2002US-0409303P.
 XX 09-APR-2003; 2003US-0461329P.
 PR (PRIM-) PRIMA INC.
 XX Galanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,
 PI Madsen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H,
 PI WPI, 2004-390329/35.
 DR N-PSDE; ADO29874.
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX Claim 151; SEQ ID NO 412; 542pp; English.
 XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancer). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 397 AA;
 SQ Query Match 98.6%; Score 2003; DB 8; Length 397;
 Best local similarity 98.7%; Pred. No. 1.7e-208;
 Matches 392; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRSPSAAMLGAAILLAASISCSGTTQGTNRSSKGRSLIGKVDGSHVTKGVTETVPS 60
 DB 1 MRSPSAAMLGAAILLAASISCSGTTQGTNRSSKGRSLIGKVDGSHVTKGVTETVPS 60
 QY 61 VDEFSASVLAGLTTVPLPIVYTVIVAVGLPSNGMALMWFLPRTKKKHPAVIYMANIALA 120
 DB 61 VDEFSASVLAGLTTVPLPIVYTVIVAVGLPSNGMALMWFLPRTKKKHPAVIYMANIALA 120
 QY 121 DLLSVTFPLKIAHYHIGNNMITYGEALCNVLIGFFGNMYCSILPMTCLSVGRWYIYVP 180
 DB 121 DLLSVTFPLKIAHYHIGNNMITYGEALCNVLIGFFGNMYCSILPMTCLSVGRWYIYVP 180
 QY 181 MGHSRKKANIAIGISLAIWLTLLVTIPLVYVKQITFIPALNITTCCHDVLPEQLLVGDMF 240
 DB 181 MGHSRKKANIAIGISLAIWLTLLVTIPLVYVKQITFIPALNITTCCHDVLPEQLLVGDMF 240
 QY 241 NYFLSLAIGVFLPAPLITASAVYLMIRLSSAMDBENSEKKRAIKLIVTVLGMYLICF 300
 DB 241 NYFLSLAIGVFLPAPLITASAVYLMIRLSSAMDBENSEKKRAIKLIVTVLGMYLICF 300
 QY 301 TFSNLLLVVHYFLIKSQGSHVYALYIVALCSTLNSCIDPFVYFVSHDFRDHAKNAL 360
 DB 301 TFSNLLLVVHYFLIKSQGSHVYALYIVALCSTLNSCIDPFVYFVSHDFRDHAKNAL 360
 QY 361 CRSVRTVKOMQVPLTSKHSRKSSSYSSSTVTYKTSY 397
 DB 361 CRSVRTVKOMQVPLTSKHSRKSSSYSSSTVTYKTSY 397

RESULT 8
 ADST74020
 ID ADST74020 standard; protein; 397 AA.
 AC ADST74020;
 DT 16-DEC-2004 (first entry)
 DE Human G-protein coupled proteinase activated receptor 2 (PAR2).
 KW Human; proteinase activated receptor 2; PAR2; G-protein coupled receptor;
 KW receptor; cardiant; neuroprotective; nephrotropic; respiratory-gen.;
 KW gastrointestinal-gen.; gene therapy.
 OS Homo sapiens.
 PN MO2004080373-A2.
 PD 23-SEP-2004.
 PF 26-FEB-2004; 2004MO-EP001896.
 PR 11-MAR-2003; 2003EP-00004980.
 PA (PARB) BAYER HEALTHCARE AG.
 PI Golz S, Brueggemeier U, Summer H;
 DR MPI: 2004-677358/66.
 DR N-PSDB; ADST74019.
 XX Screening for therapeutic agents for treating e.g., cardiovascular
 PT diseases by contacting a test compound with a proteinase activated
 PT receptor 2 (PAR2) polypeptide or polynucleotide and detecting binding of
 PT the test compound.
 PS Disclosure; SEQ ID NO 2, 121pp; English.

XX The present sequence is that of human G-protein coupled proteinase
 CC activated receptor 2 (PAR2). PAR2 is an anti-inflammatory receptor in the
 CC colon and may also play a role in the airway, regulating sodium ion
 CC absorption and anion secretion. The invention relates to novel disease
 CC associations of PAR2 polypeptides and polynucleotides. It also relates to
 CC novel methods of screening for therapeutic agents for the treatment of
 CC cardiovascular disorders, gastrointestinal and liver diseases,
 CC neurological disorders, urological disorders, haematological diseases and
 CC respiratory diseases in a mammal. Suitable therapeutic agents include a
 CC small molecule, an RNA molecule, an antisense oligonucleotide, a
 CC polypeptide, an antibody or a ribozyme. The invention also provides
 CC pharmaceutical compositions for the treatment of diseases and disorders
 CC associated with PAR2 comprising a PAR2 polypeptide, PAR2 polynucleotide
 CC or a regulator or modulator of PAR2 activity. Methods of diagnosing these
 CC diseases and disorders involve determining the amount of PAR2
 CC polynucleotide in a sample.

XX Sequence 397 AA;
 SQ Query Match 98.6%; Score 2003; DB 8; Length 397;
 Best local similarity 98.7%; Pred. No. 1.7e-208;
 Matches 392; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRSPSAAMLGAAILLAASISCSGTTQGTNRSSKGRSLIGKVDGSHVTKGVTETVPS 60
 DB 1 MRSPSAAMLGAAILLAASISCSGTTQGTNRSSKGRSLIGKVDGSHVTKGVTETVPS 60
 QY 61 VDEFSASVLAGLTTVPLPIVYTVIVAVGLPSNGMALMWFLPRTKKKHPAVIYMANIALA 120
 DB 61 VDEFSASVLAGLTTVPLPIVYTVIVAVGLPSNGMALMWFLPRTKKKHPAVIYMANIALA 120
 QY 121 DLLSVTFPLKIAHYHIGNNMITYGEALCNVLIGFFGNMYCSILPMTCLSVGRWYIYVP 180
 DB 121 DLLSVTFPLKIAHYHIGNNMITYGEALCNVLIGFFGNMYCSILPMTCLSVGRWYIYVP 180
 QY 181 MGHSRKKANIAIGISLAIWLTLLVTIPLVYVKQITFIPALNITTCCHDVLPEQLLVGDMF 240
 DB 181 MGHSRKKANIAIGISLAIWLTLLVTIPLVYVKQITFIPALNITTCCHDVLPEQLLVGDMF 240
 QY 241 NYFLSLAIGVFLPAPLITASAVYLMIRLSSAMDBENSEKKRAIKLIVTVLGMYLICF 300
 DB 241 NYFLSLAIGVFLPAPLITASAVYLMIRLSSAMDBENSEKKRAIKLIVTVLGMYLICF 300
 QY 301 TFSNLLLVVHYFLIKSQGSHVYALYIVALCSTLNSCIDPFVYFVSHDFRDHAKNAL 360
 DB 301 TFSNLLLVVHYFLIKSQGSHVYALYIVALCSTLNSCIDPFVYFVSHDFRDHAKNAL 360
 QY 361 CRSVRTVKOMQVPLTSKHSRKSSSYSSSTVTYKTSY 397
 DB 361 CRSVRTVKOMQVPLTSKHSRKSSSYSSSTVTYKTSY 397

RESULT 9
 ADL61221
 ID ADL61221 standard; protein; 397 AA.
 AC ADL61221;
 DT 03-JUN-2004 (first entry)
 DE Human coagulation factor II (thrombin) receptor-like 1 protein.
 KW predictor set; protein tyrosine kinase; cytosolic; antiangiogenic;
 KW vasotropic; vulnerary; pharmacogenomic; drug sensitivity; breast cancer;
 KW hypervascular disease; angiogenesis; wound healing scar; human;
 KW biomarker; coagulation factor II receptor-like I; thrombin; receptor.
 OS Homo sapiens.
 PN MO2004020583-A2.
 PD 11-MAR-2004.

PF	26-AUG-2003	2003MO-US026491.
XX		
PR	27-AUG-2002	2002US-0406385P.
XX		
PA	(BRIM)	BRISTOL-MYERS SQUIBB CO.
PI	Huang F, Han X, Reeves KA, Amler L, Fatchild CR, Lee FY, Shaw P;	
DR	WPI, 2004-239171/22.	
XX	N-PSDB; ADL61084.	
PT	New predictor sets with a plurality of polynucleotides and/or polypeptides whose expression pattern predicts cell response to a compound that modulates protein tyrosine kinase activity, useful in treating breast cancer.	
PS	Claim 9; SEQ ID NO 145; 643pp; English.	
XX		
CC	The invention relates to a novel predictor set comprising a plurality of polynucleotides and/or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. The molecules of the invention demonstrate cytoskeletal, antiangiogenic, vasotropic and vulnary activities and may be useful in the field of pharmacogenomics, in particular for determining drug sensitivity and in treating breast cancer, hypervascular diseases, angiogenesis and scars in wound healing. The current sequence is that of a human protein tyrosine kinase biomarker protein of the invention.	
XX		
SO	Sequence 397 AA;	
Query Match	98.4%; Score 1998; DB 8; Length 397;	
Best Local Similarity	98.5%; Pred. No. 5,9e-208;	
Matches 391; Conservative	1; Mismatches 5; Indels 0; Gaps 0	
QY	1 MRSPPAAMTLGAAITLAAISLSCSGTIOGTNRSSKGRSLIGKIDGTSHTGKAVTETVVS	60
DB	1 MRSPPAAMTLGAAITLAAISLSCSGTIOGTNRSSKGRSLIGKIDGTSHTGKAVTETVVS	60
QY	61 VDRPSASVLAGLTITVPLPIVVTIYPAVGLPENGMAWVFLPRTKKGPAVLYMANLALA	120
DB	61 VDRPSASVLAGLTITVPLPIVVTIYPAVGLPENGMAWVFLPRTKKGPAVLYMANLALA	120
QY	121 DLSATWPEPLKIAVYIHGNMVIYGBALCNVLGPFYGNMVCILFPTCLSVGRVYVYNP	180
DB	121 DLSATWPEPLKIAVYIHGNMVIYGBALCNVLGPFYGNMVCILFPTCLSVGRVYVYNP	180
QY	181 MGHSHKKANIAIGISLAIMWLTLLVTTIPLYVVKQTPIPALNITTCCHDVLPEQLLVGDMF	240
DB	181 MGHSHKKANIAIGISLAIMWLTLLVTTIPLYVVKQTPIPALNITTCCHDVLPEQLLVGDMF	240
QY	241 NYPLSLAIGVLPFAPFLTASAVVIMIRMLRSSAMENBSKKRRAIKLIVTLYAMVLCF	300
DB	241 NYPLSLAIGVLPFAPFLTASAVVIMIRMLRSSAMENBSKKRRAIKLIVTLYAMVLCF	300
QY	301 TPSNLILVVFHFLISQGSQSHVYALYVALCLSTNSCIDPFTVYFVSHDFDPAKNAAL	360
DB	301 TPSNLILVVFHFLISQGSQSHVYALYVALCLSTNSCIDPFTVYFVSHDFDPAKNAAL	360
QY	361 CRSVATVKKOVPLTSKGRSKSSSYSSSSTTVKTSY	397
DB	361 CRSVATVKKOVPLTSKGRSKSSSYSSSSTTVKTSY	397
RESULT 10		
ABP81907		
ID	ABP81907 standard; protein; 397 AA.	
XX		
AC	ABP81907;	
XX		
DT	04-MAR-2003 (first entry)	

XX Human proteinase-activated receptor 2 protein SEQ ID NO:300.
DE
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW giant versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
XX Homo sapiens.
OS
XX MOZ00261087-A2.
XX
XX PD 08-AUG-2002.
XX
XX PF 19-DEC-2001; 2001WO-US050107.
XX
XX PR 19-DEC-2000; 2000US-0257144P.
XX
XX PA (LIFEP-) LIFESPAN BIOSCIENCES INC.
XX
XX Burmer GC, Roush CL, Brown JP,
PI WPI; 2003-046718/04.
DR N-PDB; ABZ42755.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
PS Disclosure; Fig 1, 523pp; English.

The present invention describes antigenic peptides (1) comprising: (a)
any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
acids. Also described: (1) an assay for the detection of a particular G
protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
and (2) an isolated antibody having high specificity and high affinity or
avidity for a particular GPCR. (1) can be used as GPCR modulators and in
gene therapy. The antigenic peptides for GPCRs are useful in detecting an
antibody against a particular GPCR, and in the production of specific
antibodies. The peptides and antibodies are also useful for detecting the
presence or absence of corresponding GPCRs. The antigenic peptides for
GPCRs and antibodies are useful for diagnosing and designing drugs for
treating immune-related diseases, growth-related diseases, cell
regeneration-related disease, immunological-related cell proliferative
diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
atherosclerosis, bacterial, fungal, protozoan or viral infections,
osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
inflammation, allergies, Crohn's disease, diabetes, graft versus host
disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
anxiety, depression, schizophrenia, dementia, mental retardation, memory
loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
any other disorder in which GPCRs are involved. The antibodies may be
used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
GPCR proteins given in ABP81675 to ABP82019, which are used in the
exemplification of the present invention

Sequence 397 AA;

Query Match 98.3%; Score 1997; DB 6; Length 397;
Best Local Similarity 98.5%; Pred. No. 7.6e-208;
Matches 391, Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 MRSSAMTGAATLLAASCSCTTGCTGRRSSGRSLIGKVDGTSHYTKGVETVFS 60
|||||

DB 1 MRSPSAAMLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGTSHTGKVTVETFS 60
 QY 61 VDFFSASVLAGKLTIVFPIVTVIVAVGLPSNGMALWFLPRTKKGHPAVIYMANLALA 120
 DB 61 VDFFSASVLAGKLTIVFPIVTVIVAVGLPSNGMALWFLPRTKKGHPAVIYMANLALA 120
 QY 121 DLLSVIWFPLKIAIYHIGNNMIYGEALCNVLIGFPYGNMYCSILFMTCLSVGRYWIYVP 180
 DB 121 DLLSVIWFPLKIAIYHIGNNMIYGEALCNVLIGFPYGNMYCSILFMTCLSVGRYWIYVP 180
 QY 181 MGHSRKKAIAIGISLAIWMLTLVTPPLYVVKQTIFIPALNTTCHDVLPEQLVGDME 240
 DB 181 MGHSRKKAIAIGISLAIWMLTLVTPPLYVVKQTIFIPALNTTCHDVLPEQLVGDME 240
 QY 241 NYFLSLAIGVFLFPALITASAVYLMRLRSSAMDENSEKRRRAIKLIVTVLGMFLICF 300
 DB 241 NYFLSLAIGVFLFPALITASAVYLMRLRSSAMDENSEKRRRAIKLIVTVLGMFLICF 300
 QY 301 TFSNLLLVVHYFLIKSQGSHVYALYIVALCLSTLNSCIDPFYVYVSHDFRDHAKNALL 360
 DB 301 TFSNLLLVVHYFLIKSQGSHVYALYIVALCLSTLNSCIDPFYVYVSHDFRDHAKNALL 360
 QY 361 CRSVRTVKOMQVPLTSKGRSSSSSYSSSTTVKTSY 397
 DB 361 CRSVRTVKOMQVPLTSKGRSSSSSYSSSTTVKTSY 397

RESULT 11

ADK52594
 ID ADK52594 standard; protein; 397 AA.

AC ADK52594;
 XX
 XX
 DT 06-MAY-2004 (first entry)

XX Hematological disorder associated Gene ID 340 encoded protein.
 XX
 XX cytostatic; antiamebic; antischistosomal; virucide; hemostatic; nephrotoxic;
 KW cytostatic; thrombolytic; antiparasitic; gene therapy;
 KW hematologic disorder; cancer; Sickle Cell Anemia;
 KW Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;
 KW Reticuloblastoma; Hemophilia; Thrombocytopenia; Thalassemia;
 KW transfusion reaction; Erythroblastosis; mechanical trauma;
 KW micro-angiopathic hemolytic anemia; parasite infection.

OS Homo sapiens.

PN WO2003065871-A2.

PD 14-AUG-2003.

PF 28-JAN-2003; 2003WO-US002484.

PR 04-FEB-2002; 2002US-0354333P.

PR 28-FEB-2002; 2002US-0360258P.

PR 15-MAR-2002; 2002US-0364476P.

PR 26-APR-2002; 2002US-0375262P.

PR 06-JUN-2002; 2002US-0386494P.

PR 24-JUN-2002; 2002US-0390965P.

PR 28-JUN-2002; 2002US-0392480P.

PR 03-JUL-2002; 2002US-0394188P.

PR 31-JUL-2002; 2002US-0397833P.

PR 13-AUG-2002; 2002US-0403221P.

PR 30-AUG-2002; 2002US-0407045P.

PR 25-NOV-2002; 2002US-0429048P.

XX
 XX
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 XX
 PI Carol1 JM, Healy A, Weich NS, Kelly LM;
 XX
 XX WPI; 2003-731464/69.
 DR N-PSDB; ADK52593.
 XX

PT Identifying a compound capable of treating a hematologic disorder (e.g.
 PT anemia or leukemia) comprises assaying the ability of the compound to
 PT modulate the expression or activity of e.g. 131,148, 199 or 12303
 PT polypeptide or nucleic acid.

PS disclosure; SEQ ID NO 52; 232pp; English.

XX
 XX The invention relates to a method of identifying a compound capable of
 CC treating a hematologic disorder comprising assaying the ability of the
 CC compound to modulate 131,148, 199, 12303, 13906, 15513, 17822, 302, 5677,
 CC 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871,
 CC 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic
 CC acid expression or polypeptide activity, thus, identifying a compound
 CC capable of treating a hematologic disorder. The methods are useful in
 CC diagnosing, preventing and treating hematological disorders, such as
 CC cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia,
 CC polycythemia Vera, Lymphoma, Reticuloblastoma, Hemophilia, disorders
 CC associated with an increased risk of thrombosis, Herpes, Thalassemia,
 CC antibody-mediated disorders such as transfusion reactions and micro-
 CC erythroblastosis, mechanical trauma to red blood cells such as micro-
 CC angioaphic hemolytic anemias, infections by parasites or chemical
 CC injuries. The methods may also be used for identifying compounds that
 CC modulate hematological disorders. This sequence corresponds to the
 CC protein encoded by one of the genes modulated by the compounds.

XX Sequence 397 AA;

Query Match 98.3%; Score 1997; DB 7; Length 397;

Best Local Similarity 98.5%; Pred. No. 7; 6e-208; Indels 0; Gaps 0;

Matches 391; Conservative 0; Mismatches 6;

QY 1 MRSPSAAMLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGTSHTGKVTVETFS 60
 DB 1 MRSPSAAMLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGTSHTGKVTVETFS 60
 QY 61 VDFFSASVLAGKLTIVFPIVTVIVAVGLPSNGMALWFLPRTKKGHPAVIYMANLALA 120
 DB 61 VDFFSASVLAGKLTIVFPIVTVIVAVGLPSNGMALWFLPRTKKGHPAVIYMANLALA 120
 QY 121 DLLSVIWFPLKIAIYHIGNNMIYGEALCNVLIGFPYGNMYCSILFMTCLSVGRYWIYVP 180
 DB 121 DLLSVIWFPLKIAIYHIGNNMIYGEALCNVLIGFPYGNMYCSILFMTCLSVGRYWIYVP 180
 QY 181 MGHSRKKAIAIGISLAIWMLTLVTPPLYVVKQTIFIPALNTTCHDVLPEQLVGDME 240
 DB 181 MGHSRKKAIAIGISLAIWMLTLVTPPLYVVKQTIFIPALNTTCHDVLPEQLVGDME 240
 QY 241 NYFLSLAIGVFLFPALITASAVYLMRLRSSAMDENSEKRRRAIKLIVTVLGMFLICF 300
 DB 241 NYFLSLAIGVFLFPALITASAVYLMRLRSSAMDENSEKRRRAIKLIVTVLGMFLICF 300
 QY 301 TFSNLLLVVHYFLIKSQGSHVYALYIVALCLSTLNSCIDPFYVYVSHDFRDHAKNALL 360
 DB 301 TFSNLLLVVHYFLIKSQGSHVYALYIVALCLSTLNSCIDPFYVYVSHDFRDHAKNALL 360
 QY 361 CRSVRTVKOMQVPLTSKGRSSSSSYSSSTTVKTSY 397
 DB 361 CRSVRTVKOMQVPLTSKGRSSSSSYSSSTTVKTSY 397

RESULT 12

ADN39997
 ID ADN39997 standard; protein; 397 AA.

AC ADN39997;

DT 17-JUN-2004 (first entry)

XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C367.

XX Human; differential expression; cancer; angiogenic disorder;

KW fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;
 KW inflammatory disease; autoimmune disease;

KM retinal neovascularization syndrome; scarring; uterine fibroid;
 KM detection; diagnosis; prognosis; drug screening; drug targeting;
 KM wound healing; contraception; cytostatic; cardiac; immunomodulatory;
 KM vulnerrary; gene therapy; vaccine.
 OS Homo sapiens.
 XX MO2003042661-A2.
 PN 22-MAY-2003.
 XX 13-NOV-2002; 2002MO-US036810.
 XX 13-NOV-2001; 2001US-0350666P.
 PR 21-NOV-2001; 2001US-0332464P.
 PR 29-NOV-2001; 2001US-0334393P.
 PR 03-DEC-2001; 2001US-0335394P.
 PR 14-DEC-2001; 2001US-0340376P.
 PR 08-JAN-2002; 2002US-0347211P.
 PR 10-JAN-2002; 2002US-0347349P.
 PR 08-FEB-2002; 2002US-0355250P.
 PR 13-FEB-2002; 2002US-0356714P.
 PR 20-FEB-2002; 2002US-0359077P.
 PR 29-MAR-2002; 2002US-0368809P.
 PR 04-APR-2002; 2002US-0370110P.
 PR 12-APR-2002; 2002US-0372246P.
 PR 05-JUN-2002; 2002US-0386149P.
 PR 16-JUL-2002; 2002US-0396839P.
 PR 22-JUL-2002; 2002US-0397755P.
 PR 22-JUL-2002; 2002US-0397845P.
 PR 09-SEP-2002; 2002US-0409450P.
 XX (EOB-) EOS BIOTECHNOLOGY INC.
 PA Afar D, Aziz N, Gineburg WM, Gish KC, Glynn R, Hevezi PA;
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlocznik A;
 XX MPI; 2003-468649/44.
 DR N-PSDB; ADN39780.
 XX Determining the presence or absence of a pathological cell in a patient,
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting
 PT a nucleic acid in a biological sample.
 XX Claim 12; SEQ ID NO C367; 1385bp; English.
 PS The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
 XX whose expression is upregulated or downregulated in specific cancers or
 XX other diseases such as angiogenic or fibrotic disorders, and to methods
 CC of determining the presence or absence of a pathological cell in a
 CC patient by detecting a nucleic acid at least 80% identical to those of
 CC the invention or by detecting a polypeptide of the invention. The
 CC invention also relates to expression vectors and host cells comprising a
 CC nucleic acid of the invention; antibodies which specifically bind a
 CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
 CC neovascularization syndromes, scarring and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a polypeptide of the invention.
 CC Sequence 397 AA;
 SQ
 Query Match 98.3%; Score 1997; DB 7; Length 397;
 Best Local Similarity 98.5%; Pred. No. 7.6e-208; Indels 0; Gaps 0;
 Matches 391; Conservative 0; Mismatches 6;
 1 MSPSAAMLGAILLAASLSCGTTGTRSSKGRSLGKVDGTSHTGKGVTVETVPS 60
 1 MSPSAAMLGAILLAASLSCGTTGTRSSKGRSLGKVDGTSHTGKGVTVETVPS 60

QY VDEFSASVLAGKLTTFVFLPIVYTIIVFVGLPSNGMALMVELPRTKKGPVAVIYMANLATA 120
 DB 61 VDEFSASVLAGKLTTFVFLPIVYTIIVFVGLPSNGMALMVELPRTKKGPVAVIYMANLATA 120
 QY DLLSVIWPFLKIAVYHIGNNMVIGBALCNVLIGFPGNMVCSILFMTCLSVGRVWYVNP 180
 DB 121 DLLSVIWPFLKIAVYHIGNNMVIGBALCNVLIGFPGNMVCSILFMTCLSVGRVWYVNP 180
 QY DLSVIMWFLKIAVYHIGNNMVIGBALCNVLIGFPGNMVCSILFMTCLSVGRVWYVNP 180
 DB 121 DLSVIMWFLKIAVYHIGNNMVIGBALCNVLIGFPGNMVCSILFMTCLSVGRVWYVNP 180
 QY MGRSRKANAIAGISLAIWLTLLVITPLVYVQGITIPALNITTTCHDVLPBOLLVDMF 240
 DB 181 MGRSRKANAIAGISLAIWLTLLVITPLVYVQGITIPALNITTTCHDVLPBOLLVDMF 240
 QY NYFLSLAIGVFLPAPFLTASAVYLMIRMLSSAMDESEKGRRAIKLYTVYGMYLICF 300
 DB 241 NYFLSLAIGVFLPAPFLTASAVYLMIRMLSSAMDESEKGRRAIKLYTVYGMYLICF 300
 QY TPNLNLVYHYFLIKSGQSHVVALYIVLCLSTLNSCIDPFYVYVSHDFRDHAKNAL 360
 DB 301 TPNLNLVYHYFLIKSGQSHVVALYIVLCLSTLNSCIDPFYVYVSHDFRDHAKNAL 360
 QY CRSVRTVKQWQVPLTSKGRSSSYSSSSTTYKTSY 397
 DB 361 CRSVRTVKQWQVPLTSKGRSSSYSSSSTTYKTSY 397
 RESULT 13
 ADR46675
 ID ADR46675 standard; protein, 397 AA.
 AC ADR46675;
 XX 18-NOV-2004 (first entry)
 DT Cancer-associated protein, SEQ ID 88.
 DE Cytostatic; Gene Therapy; cancer; human.
 KM Homo sapiens.
 OS Homo sapiens.
 XX MO2004073657-A2.
 PN 02-SEP-2004.
 PD 19-FEB-2004; 2004MO-US005455.
 PP 19-FEB-2003; 2003US-0448784P.
 PR (PROT-) PROTEIN DESIGN LABS INC.
 PA Aziz N, Gish KC, Wilson KE, Zlocznik A;
 PI MPI; 2004-652787/63.
 DR N-PSDB; ADR46617.
 XX Detecting a pathological cell in a patient for diagnosing or treating
 PT cancer by detecting in a biological sample from the patient genes whose
 PT expression are up-regulated or down-regulated in specific cancers.
 XX Claim 1; SEQ ID NO 88; 375bp; English.
 PS The present invention relates to a method for detecting cancer in a
 CC patient. The method comprises detecting in a biological sample from the
 CC patient a nucleotide or protein sequence comprising a sequence that is at
 CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
 CC protein sequence (ADR46646-ADR46703). The method is useful for detecting
 CC cancer for preparing a composition for diagnosing or treating cancer.
 CC Sequence 397 AA;
 SQ
 Query Match 98.3%; Score 1997; DB 8; Length 397;
 Best Local Similarity 98.5%; Pred. No. 7.6e-208;
 Matches 391; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSPPSAAMLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 CC 1 MSPPSAAMLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 XX 1 MSPPSAAMLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 Db 61 VDEFSASVLAGKLTTFPLPIVTTIVPAVGLPSNGMALWFLFRTKKKHPAVIYMANLALA 120
 QY 121 DLSVWMPFLKTAHYHGNWNYGKALCNVLIGFFGNMYCSILFMTCLSVORWYVNP 180
 Db 121 DLSVWMPFLKTAHYHGNWNYGKALCNVLIGFFGNMYCSILFMTCLSVORWYVNP 180
 QY 181 MGSRRKANAIGISLAIMLTLVTIPLYVVKQTFIPALNITTCADVLPBQLVGDME 240
 Db 181 MGSRRKANAIGISLAIMLTLVTIPLYVVKQTFIPALNITTCADVLPBQLVGDME 240
 QY 241 NYFLSLAIGVFLPPALFASAVYLMIRLSSAMDNSSEKKRAIKLIVTVLGMFLICF 300
 Db 241 NYFLSLAIGVFLPPALFASAVYLMIRLSSAMDNSSEKKRAIKLIVTVLGMFLICF 300
 QY 301 TSENLLVHYHFLIKSQGSHVYALYVALCTLNSCIDPFYVYFVSHDFRDHAKNALL 360
 Db 301 TSENLLVHYHFLIKSQGSHVYALYVALCTLNSCIDPFYVYFVSHDFRDHAKNALL 360
 QY 361 CRSVRTKQMOVPLTSKGRSKSSSYSSSTTVKTSY 397
 Db 361 CRSVRTKQMOVPLTSKGRSKSSSYSSSTTVKTSY 397
 RESULT 14
 AAM51408
 ID AAM51408 standard; protein; 394 AA.
 XX AAM51408;
 AC AAM51408;
 XX 12-OCT-1998 (first entry)
 DT 12-OCT-1998 (first entry)
 XX Human protease-activated receptor 2 (PAR2).
 DE Human protease-activated receptor 2 (PAR2).
 XX Protease-activated receptor 2; PAR2; PAR3; thrombin receptor; human.
 KM Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Cleavage-site 36..37
 FT /note="thrombin cleavage site"
 FT
 XX MO9818456-A1.
 PN 07-MAY-1998.
 XX 29-OCT-1997; 97MO-US019732.
 XX 30-OCT-1996; 96US-00742440.
 PR (REGC) UNIV CALIFORNIA.
 XX Coughlin SR, Ishihara H, Connolly A;
 PI WPI, 1998-271905/24.
 DR
 XX DNA encoding protease-activated receptor 3 - for detection of specific
 PT agonists and antagonists, potentially useful for treating e.g.
 PT thrombosis, atherosclerosis, inflammation etc.
 XX Example 1; Page 43-44; 74pp; English.
 PS This polypeptide comprises human protease-activated receptor 2 (PAR2).
 CC The physiological activator of PAR2 remains unknown; it is not activated
 CC by thrombin. The invention relates to novel mouse and human PAR3 (see
 CC AAM51405-06) that show homology to PAR2 and which are specific receptors
 CC for thrombin. They can be used to screen for specific agonists and

CC antagonists of thrombin useful e.g. for treating atherosclerosis,
 CC thrombosis and inflammation
 XX Sequence 394 AA;
 SQ
 Query Match 96.8%; Score 1965.5; DB 2; Length 394;
 Best Local Similarity 97.7%; Pred. No. 2e-204;
 Matches 388; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
 QY 1 MSPPSAAMLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 Db 1 MSPPSAAMLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 QY 61 VDEFSASVLAGKLTTFPLPIVTTIVPAVGLPSNGMALWFLFRTKKKHPAVIYMANLALA 120
 Db 61 VDEFSASVLAGKLTTFPLPIVTTIVPAVGLPSNGMALWFLFRTKKKHPAVIYMANLALA 120
 QY 121 DLSVWMPFLKTAHYHGNWNYGKALCNVLIGFFGNMYCSILFMTCLSVORWYVNP 180
 Db 121 DLSVWMPFLKTAHYHGNWNYGKALCNVLIGFFGNMYCSILFMTCLSVORWYVNP 180
 QY 181 MGSRRKANAIGISLAIMLTLVTIPLYVVKQTFIPALNITTCADVLPBQLVGDME 240
 Db 181 MGSRRKANAIGISLAIMLTLVTIPLYVVKQTFIPALNITTCADVLPBQLVGDME 240
 QY 241 NYFLSLAIGVFLPPALFASAVYLMIRLSSAMDNSSEKKRAIKLIVTVLGMFLICF 300
 Db 240 - FLSLAIGVFLPPALFASAVYLMIRLSSAMDNSSEKKRAIKLIVTVLGMFLICF 297
 QY 301 TSENLLVHYHFLIKSQGSHVYALYVALCTLNSCIDPFYVYFVSHDFRDHAKNALL 360
 Db 298 TSENLLVHYHFLIKSQGSHVYALYVALCTLNSCIDPFYVYFVSHDFRDHAKNALL 357
 QY 361 CRSVRTKQMOVPLTSKGRSKSSSYSSSTTVKTSY 397
 Db 358 CRSVRTKQMOVPLTSKGRSKSSSYSSSTTVKTSY 394
 RESULT 15
 ADO28601
 ID ADO28601 standard; protein; 389 AA.
 XX ADO28601;
 AC ADO28601;
 XX 12-AUG-2004 (first entry)
 DT 12-AUG-2004 (first entry)
 XX Human PAR2 protein SEQ ID NO:30.
 DE Human PAR2 protein SEQ ID NO:30.
 XX high-grade dysplasia; KGD; oesophageal adenocarcinoma;
 KW neo-plastic transformation; cancer; cytostatic; gene therapy; human;
 XX PAR2; chromosome 5.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH MISC-difference 44
 FT /note="encoded by ACATCC"
 FT MISC-difference 101
 FT /note="encoded by CGAAGT"
 FT MISC-difference 158
 FT /note="encoded by TGTTC"
 FT MISC-difference 215
 FT /note="encoded by CCTGCC"
 FT MISC-difference 272
 FT /note="encoded by AACTCA"
 FT MISC-difference 329
 FT /note="encoded by CTTAAC"
 FT MISC-difference 386
 FT /note="encoded by GTTAAG"
 XX MO2004044178-A2.
 XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036260.
PF
XX
PR 13-NOV-2002; 2002US-0425813P.
XX
PA (GETH) GENENTECH INC.
XX
PI Smith V;
XX
DR MPI, 2004-420319/39.
XX
DR N-PSDB; ADO28600.
XX
PT Detecting of high-grade dysplasia in cells of a mammalian tissue sample
PT comprises establishing the level of expression in the test tissue sample
PT of the gene.
XX
XX
PS Disclosure; SEQ ID NO 30; 256pp; English.
XX
XX
CC The present invention describes a method for detecting high-grade
CC dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
CC (1) identifying an oesophageal tissue susceptible to oesophageal
CC adenocarcinoma; (2) determining the predisposition of a mammalian tissue
CC to a neo-plastic transformation by detecting HGD in cells of the tissue;
CC and (3) detecting cancer in a patient. The method can be used in
CC detecting HGD and cancer in cells of a mammalian tissue sample. The
CC methods and compositions of the present invention can be used in treating
CC and preventing HGD and cancer, and in gene therapy. The present sequence
CC represents human PAR2, which is used in the exemplification of the
CC present invention. The human PAR2 gene is located on chromosome 5.
XX
XX
SQ Sequence 389 AA;

Query Match 92.8%; Score 1884.5; DB 8; Length 389;
Best Local Similarity 97.0%; Pred. No. 1.3e-195;
Matches 384; Conservative 0; Mismatches 5; Indels 7; Gaps 7;

QY 2 RSPSAAMLGAATLLAASISCSGTIOGTNRSSKGRSLIGKVDGTSHTYKGVTVETVFSV 61
DB 1 RSPSAAMLGAATLLAASISCSGTIOGTNRSSKGRSLIGKVDG-SHTYKGVTVETVFSV 59
QY 62 DEFSASVLAGKLTTPVLPVYTVFPAVGLPSNGMALWFLFRTKQKPAVIYMANLALAD 121
DB 60 DEFSASVLAGKLTTPVLPVYTVFPAVGLPSNGMALWFLF-TKQKPAVIYMANLALAD 118
QY 122 LLSVTFPLKIAVHIGNMWYIGBALCNVLIGFFYGMYSIIPTCLSVQRYWVYNPM 181
DB 119 LLSVTFPLKIAVHIGNMWYIGBALCNVLIGFFYGMYS-SIIPTCLSVQRYWVYNPM 177
QY 182 GHSRKKANIAIGSLAIWLTLLVTTPVLYVVKOTIFIPALNITTCDDVLPQOLLVGDMPN 241
DB 178 GHSRKKANIAIGSLAIWLTLLVTTPVLYVVKOTIFP-ALNITTCDDVLPQOLLVGDMPN 236
QY 242 YPLSLAIGVFLPAPFLTASAYVLMIRMSAMDENSEKKRAIKLIIVTLGMYLICFT 301
DB 237 YPLSLAIGVFLPAPFLTASAYVLMIRMSAMDENSEKKRAIKLIIVTLGMYLICFT 295
QY 302 PSNLLVVRHFFLIKSQGSQSHVYALYVALCLSTLNSCIDPPVTFYVSHDFRDHAKNALC 361
DB 296 PSNLLVVRHFFLIKSQGSQSHVYALYVALCLST-NSCIDPPVTFYVSHDFRDHAKNALC 354
QY 362 RSVRTVKOMQVPLTSKGRSKRSSYSSSSTTVTKTSY 397
DB 355 RSVRTVKOMQVPLTSKGRSKRSSYSSSSTTVTKTSY 389

Search completed: March 18, 2005, 21:06:44
Job time : 69.9132 secs

